DENTAL ANALYSIS OF CLASSIC PERIOD POPULATION VARIABILITY IN THE MAYA AREA

A Dissertation

by

ANDREW KENNETH SCHERER

Submitted to the Office of Graduate Studies of
Texas A&M University
in partial fulfillment of the requirements for the degree of

DOCTOR OF PHILOSOPHY

December 2004

Major Subject: Anthropology

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Approved as to style and content by:

Lori E. Wright (Chair of Committee)	D. Gentry Steele (Member)
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ABSTRACT

Dental Analysis of Classic Period Population Variability in the Maya Area.

(December 2004)

Andrew Kennerth Scherer, B.A., Hamline University

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In this dissertation I examine population history and structure in the Maya area during the Classic period (A.D. 250-900). Within the Maya area, archaeologists have identified regional variation in material culture between archaeological zones. These cultural differences may correspond to biological differences between Classic Maya populations. I test the hypothesis that Classic Maya population structure followed an isolation by distance model. I collected dental nonmetric and metric traits on 977 skeletons, from 18 Classic period sites, representing seven different archaeological zones. I corrected the data for intraobserver error. For the dental nonmetric data, I developed a Maya-specific trait dichotomization scheme and controlled for sex bias. I tested the dental metric data for normality and age affects. I imputed missing dental metric data for some traits and the remaining set of traits was Q-mode transformed to control for allometric factors. I analyzed the dental nonmetric and metric datasets with both univariate and multivariate tests. I found, with a log likelihood ratio, that 50% of the nonmetric traits exhibited statistically significant differences between Maya sites. I performed a Mean Measure of Divergence analysis of the dental nonmetric dataset and found that majority of the resulting pairwise distance values were significant. Using cluster analysis and multidimensional scaling, I found that the dental nonmetric data do not support an isolation by distance organization of Classic Maya population structure. In the ANOVA and MANOVA tests, I did not find major statistically significant differences in dental metrics between Maya

sites. Using principal components analysis, a Mahalanobis Distance test, and **R** matrix analysis, I found a generally similar patterning of the dental metric data. The dental metric data to not support an isolation by distance model for Classic Maya population structure. However, the geographically outlying sites from Kaminaljuyu and the Pacific Coast repeatedly plotted as biological outliers. **R** matrix analysis indicates that gene flow, not genetic drift, dominated Classic Maya population structure. Based on the results of the dental nonmetric and metric analyses, I reject the hypothesis that isolation by distance is a valid model for Classic Maya population structure. From the multivariate analyses of the dental nonmetric and metric data, a few notable observations are made. The major sites of Tikal and Calakmul both demonstrate substantial intrasite biological heterogeneity, with some affinity to other sites but with little to one another. Piedras Negras demonstrates some evidence for genetic isolation from the other lowland Maya sites. In the Pasión Zone, Seibal and Altar de Sacrificios demonstrate some affinity to one another, though Dos Pilas is an outlier. The **R** matrix analysis found evidence of Classic period immigration into Seibal from outside the network of sites tested. The Belize Zone exhibited substantial heterogeneity among its sites, with the site of Colha showing some affinity to the Central Zone. Copan, despite being a geographic outlier, demonstrates genetic affinity with the rest of the Maya area. Kaminaljuyu and the Pacific Coast were both found to be outliers. These results indicate that dental nonmetric and metric data are a useful tool for investigating ancient biological variability in the Maya area and contribute to our expanding understanding of population history in that region.

This research is dedicated to my parents,

for their infinite support throughout this endeavor.

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I would also like to thank my former professors at Hamline University for providing an excellent undergraduate education in anthropology and more than adequately preparing me for the rigors of graduate school. I am indebted to Barbara O'Connell for introducing me to the exciting field of bioarchaeology and convincing me that teeth were not so bad after all. Susan Myster continued that education and introduced me to biological distance research through her own work on the biological affinities of Midwest American Indians. Lewis "Skip" Messenger gave me my introduction to Maya archaeology. It was during January of 1997, while writing a final exam for Skip in a hotel in Merida, Mexico that this dissertation project was first conceived.

I would like to acknowledge the tremendous assistance of the following institutions and individuals who graciously facilitated my study of the skeletal collections under their supervision: Héctor Escobedo of the Universidad del Valle and Stephen Houston of Brigham

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CHAPTER I

INTRODUCTION

> In the midst of desolation and ruin we looked back to the past, cleared away the gloomy forest, and fancied every building perfect, with its terraces and pyramids, its sculptured and painted ornaments, grand, lofty, and imposing, and overlooking an immense inhabited plain; we called back into life the strange people who gazed at us in sadness from the walls; pictured them, in fanciful costumes and adorned with plumes of feathers, as ascending the terraces of the palace and the steps leading to the temples. Nothing ever impressed me more forcibly than the spectacle of this once great and lovely city, overturned, desolate, and lost; discovered by accident, overgrown with trees for miles around, and without even a name to distinguish it.
>
> John Lloyd Stephens, 1841

Stephens' description of the ruins of Palenque, over a century and a half ago, still resonates today. Ever since Stephens wrote of his travels to the lost cities of Mexico, Guatemala, and Honduras, the Maya have fascinated scholar and amateur alike. At its height during the Classic period, from A.D. 250 to 900, ancient Maya civilization was one of the most complex societies in the world. During their time, the Classic Maya had few equals. They developed a complex system of agriculture that permitted them to feed cities in the thousands and tens of thousands. Maya artisans achieved an unparalleled level of skill in art. The Maya developed the only true indigenous written language in the New World. Maya architects constructed some of the largest and most complex structures in Precolumbian America. Yet by the end of the ninth century, much of Classic Maya civilization was in ruin.

With the advent of modern archaeology, researchers have devoted a tremendous amount of time and money to understanding how ancient Maya cities developed and why so many of them were abandoned abruptly in the ninth century. Central to this research is an understanding of ancient Maya population history. Where did the Maya come from? How did they interact

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This dissertation follows the style and format of *American Antiquity*.

with one another? How were their cities related? What populations were they in contact with outside of the Maya area? How large were ancient Maya populations? What ultimately happened to the Classic period populations? These and other questions have fueled Maya archaeology for decades.

In order to address issues pertaining to population history, Mayanists have used a battery of research tools. The study of ceramics, both typological and chemical, has proven a fruitful means for constructing temporal chronologies at Maya sites and understanding interactions between them (Foias 2004). The analysis of settlement at Maya sites has permitted demographic reconstructions, including estimates of population size and its change through time (Culbert and Rice 1990). The decipherment of Classic period hieroglyphs has opened a window on ancient Maya history and socio-political interaction and allows us to date certain events to the very day they occurred (M. Coe 1999; Martin and Grube 2000).

Ignored until recently, was data obtained from the ancient Maya themselves—from the bones and burials that are ubiquitous throughout Maya sites. Largely due to the landmark studies by Haviland (1967) on stature at Tikal and paleopathogy a Altar de Sacrificios (Saul 1972), more and more Mayanists are turning to skeletal remains to learn about ancient Maya populations. Much of this research had been devoted to health, disease, and diet and how these factors may have contributed to the collapse of Maya society. (Danforth 1994, 1997, 1999; Reed 1998; Saul 1975; Storey 1997, 1999; Tiesler 1999; White 1986, 1988, 1997; Whittington 1989, 1999; Whittington and Reed 1997; Wright 1994, 1997a, b; Wright and White 1996). Far less prominent, though nonetheless important, are studies of Maya skeletons that address issues of population history and structure (Austin 1978; Cucina and Tiesler 2004; Jacobi 2000; Pompa y Podilla 1990; Rhoads 2002; Wrobel 2003).

The comparison of morphological and metric characteristics of the skeleton and teeth among different skeletal populations has a long history in physical anthropology. Commonly referred to as biological distance, this research has been used to address a breadth of issues, from the peopling of the New World (Steele and Powell 1999; Turner 1986) to population structure in post-famine Ireland (Relethford 1991; Relethford, et al. 1997). The driving theory of biological distance research is that biological affinity can be inferred from levels of phenotypic similarity between skeletal populations—those that are morphometrically similar are so because of shared ancestry and/or gene flow (Buikstra, et al. 1990). More recently, biological distance studies have become far more sophisticated and complicated, borrowing method and theory from the field of population genetics (Konigsberg 1990a; Powell and Neves 1999; Relethford and Blangero 1990).

In this dissertation, I bring the methods of biological distance to bear on questions pertaining to ancient Maya population history. Previous work on biological distance in the Maya area has been limited to intrasite analyses (Jacobi 2000; Rhoads 2002) or to analyses of a few sites from a limited number of archaeological zones (Austin 1978; Cucina and Tiesler 2004; Pompa y Podilla 1990; Wrobel 2003). I use data from 977 dentitions, from 18 Classic period sites, that represent seven different archaeological zones. The central question of this research is to determine whether Classic Maya population structure fits an isolation by distance model. This hypothesis assumes that the regional variation we see in Classic Maya material culture is due to limited interaction, in both a cultural and biological sense, between sites of different archaeological zones. If this hypothesis is rejected, I will use the biological data, in conjunction with the archaeological and hieroglyphic records, to develop an alternative model for Classic Maya population structure and history. I use both dental nonmetric and metric data in this dissertation and I employ statistical methods commonly referred to in the physical anthropology

literature as "model-bound" and "model-free" approaches to biological variability (Relethford and Lees 1982).

Although model-free statistics have a long history of use in osteological studies, model-bound statistics are relatively new and have only been applied in bioarchaeological research on the peopling of the New World (Powell and Neves 1999), precontact Midwest America (Konigsberg 1988, 1990b; Konigsberg and Buikstra 1995; Steadman 1998, 2001), and colonial southeastern United States (Stojanowski 2003a, b, 2004). This study provides a unique opportunity to examine how model-free and model-bound approaches perform in a bioarchaeological study of a complex society, like that of the ancient Maya. One benefit of conducting biological distance research on the ancient Maya is that skeletal samples at some sites are relatively large and ancient population sizes can be estimated with reasonable accuracy. As a result, this research will contribute both to the fields of Maya archaeology and physical anthropology.

In Chapter II, I provide an overview of ancient Maya culture, focusing on Preclassic and Classic period developments. I then discuss our current knowledge of Maya population history, as is known for each of the archaeological zones addressed in this dissertation.

I present the research hypotheses and biological models that form the basis of this dissertation in Chapter III. I also discuss the theory behind using skeletal samples to reconstruct ancient population variation, and discuss some of the caveats involved in these types of investigations.

I provide a background on previous research on ancient human population variation in Chapter IV, including earlier work in the Maya area. This discussion focuses on dental metric and nonmetric analyses, the type of biological data used in this research. In this review, I discuss

some of the differences in what have been termed “model-free” and “model-bound” approaches to population variability.

In Chapter V, I present information about the ancient Maya skeletal samples used in this analysis. I explain how age and sex was determined for each sample and what sources were used to obtain mortuary context data for the skeletal samples. I also discuss how population estimates were derived for each site in this analysis and how I determined my own population ranks to be used in the **R** matrix analyses in Chapter VII.

I present the methods and results of the dental nonmetric analysis in Chapter VI. I detail the methods and results of the dental metric analysis in Chapter VII. In Chapter VIII, I discuss the implications of this research, reviewing what the data tell us about the research questions and hypotheses originally presented in Chapter III. In my conclusions, I discuss both the results of this study and offer suggestions for future research.

CHAPTER II

THE ANCIENT MAYA

The purpose of this chapter is to provide an overview of the ancient Maya, with an emphasis on population history. First, I provide a brief introduction to the Maya world. I then proceed to a review of the archaeology of the Maya area. This discussion is organized by archaeological zone. Archaeological zones are regions that are distinguished from one another by differences in material culture, settlement patterns, and general historical trajectories (Culbert 1973b; Hammond 1991b; Marcus 1993). In this discussion, I emphasize issues pertaining to population history. Particular attention is paid to chronological information about when populations developed and declined in each archaeological zone, interactions between zones, and evidence of gene flow and migration during the Classic period.

THE MAYA AREA: THROUGH SPACE AND TIME

The Maya region is part of the larger Mesoamerican culture area that is defined by a number of characteristics, including an agricultural subsistence system (emphasizing maize, beans, squash and other crops), the presence of complex societies centered around urban or semi-urban centers, monumental architecture, calendrical systems, the ball game, human sacrifice, and, in some cases, the presence of writing (Kirchoff 1952). The Maya area is located in the eastern portion of Mesoamerica. Archaeologically, the Maya are best known from their Classic period (A.D. 250-900) art, architecture, and writing.

Today, the word "Maya" refers to a collection of linguistically and culturally related people who inhabit Guatemala, Belize, eastern Mexico, and the western portions of Honduras and El Salvador. Generally speaking, the archaeologically defined Maya region corresponds to

the modern day distribution of Maya-speakers. Scholars divide the Maya archaeological area into three regions: (1) the lowlands of northern Guatemala, western Honduras, Belize, and eastern Mexico, (2) the highlands of Guatemala and Chiapas, and (3) the Pacific Coast of Guatemala and Chiapas.

The term "Maya" is derived from the name by which the inhabitants of the Yucatán called themselves at the time of Spanish contact (Webster 2002: 38). The Spaniards in turn applied this term to all of the Indian populations of eastern Mesoamerica. Nonetheless, all of the cultural groups identified today as "Maya" demonstrate significantly more linguistic similarity to one another than any of these groups do to languages elsewhere in Mesoamerica (Greenberg 1987). Although, the distribution of the modern Maya generally corresponds to the archaeologically defined ancient Maya culture region, it is doubtful that the ancient people who inhabited the region we now know as the Maya area saw themselves as part of a collective whole. Nonetheless, as Webster (2002: 46) aptly points out, even though the concept of a "Maya civilization" was first born out of the writings of John Lloyd Stephens and other early Euro-American explorers, there nonetheless exists a similarity in cultural behavior and language across the Maya region to warrant its use as a concept.

A number of cultural features were characteristic of the Maya during the Classic period. One of the most salient is the use of hieroglyphic writing. Sites across Maya heartland all used a common hieroglyphic script, which epigraphers and linguists argue most closely resembles the modern Ch'olan languages (Houston, Robertson, et al. 2000). Another important unifying characteristic of the ancient Maya was a shared religious system, centered in part on a creation myth best known to us today from the 16th century Quiché *Popol Vuh* (Tedlock 1985), but traceable as far back as the Late Preclassic period as demonstrated in the recently discovered murals of San Bartolo (Saturno and Taube 2004).

Most archaeologists recognize three major time periods in the Maya area: the Preclassic period (2000 B.C. to A.D. 250), the Classic period (A.D. 250 to 900), and the Postclassic period (A.D. 900 to 1500) (Table 2.). Although these time periods are etic designations made by modern archaeologists, they nonetheless correspond to major cultural transformations in Maya history.

The earliest evidence for humans in the region comes from Clovis points dating to around 8000-9000 B.C. from the highlands of Guatemala (M. D. Coe 1999). Like the rest of the Americas, these early settlers of the region were nomadic hunter gatherers. The Archaic period (ca. 6000-2000 B.C.) saw the appearance of the first sedentary villages in the Maya region. At these early communities, archaeologists have uncovered evidence for early plant domestication, including maize (Pope, et al. 2001).

During the Early Preclassic period (2000-1000 B.C.), a rise in social complexity occurred at sites in the Soconusco region of the Pacific Coast of Chiapas and Guatemala (Clarke and Blake 1994). This includes the appearance of an elite ruling class, distinguished from commoners by the appearance of prestige artifacts. During the Middle Preclassic period (1000 B.C. to 400 B.C.), the Pacific Coast remained an important area of settlement (Bove 1989b; Voorhies 1989). However, major sections of the lowlands also appear to have been settled during this time, perhaps by migrants from the highlands (Andrews V 1990). By the end of the Middle Preclassic period, some of the earliest major lowland Maya centers, such as Nakbe and El Mirador, rose to prominence in the seemingly unlikely locale of the

Table 2.1. Chronology of the Maya area.

Period	**Dates**
Postclassic	
Late	A.D. 1250 – 1519
Early	A.D. 1000 – 1250
Classic	
Terminal	A.D. 800 – 900
Late	A.D. 600 – 800
Early	A.D. 250 – 600
Preclassic	
Late	400 B.C. – A.D. 250
Middle	1000 – 400 B.C.
Early	2000 – 1000 B.C.

tropical forest of northern Guatemala (Dahlin 1984; Matheny 1987). Both Nakbe and El Mirador feature monumental architecture (some of the largest ever constructed in the Maya lowlands) and dense populations.

By the Late Preclassic period (400 B.C – A.D. 250), the roots of Maya civilization were fully realized. During this time, sites across the Maya region increased in complexity and the first true Maya urban centers appeared (Freidel, et al. 2002). It is also during the Late Preclassic period that hieroglyphic writing appeared in the lowlands, accompanied by the Maya Long Count. Powerful Late Preclassic Maya centers were situated across the region, including El Mirador, Nakbe, Cuello, and Cerros in the lowlands; Kaminaljuyu in the Guatemalan Highlands; and the sites of Izapa, Abaj Takalik and El Baúl along the Pacific Coast. Many of the major Classic period sites, such as Tikal, Calakmul, Uaxactun, Lamanai, Seibal, and Altar de Sacrificios were developing into significant centers during the Late Preclassic period. Other major Classic period sites, however, were still villages during the Preclassic period, including Piedras Negras and Palenque.

At the close of the Late Preclassic period, some prominent sites, such as El Mirador and Nakbe fell into decline, and other sites, such as Cerros and Cuello, were completely abandoned (Hansen 2001). At the same time, other centers began to grow in size and importance. Undoubtedly, these shifts in fortune were accompanied by major population movements. Although the Late Preclassic – Early Classic transition is as poorly understood as the Classic Collapse, archaeologists have offered a number of hypotheses to explain the transition. One notable event is the eruption of Ilopango volcano in El Salvador that possibly affected crop production in the southern Maya area (Sheets 1987). However, other factors must have been at work, since a number of sites in northern Guatemala and Belize, hundreds of kilometers to the north of the volcano, went into decline and were abandoned. As an alternative, endemic warfare

has been offered as an explanation for the collapse of many of the Preclassic sites (Hansen 2001).

The Classic period (A.D. 250 – 600) marks the fluorescence of ancient Maya civilization. It is during this time period that the Maya reached their apogee. Archaeologists divide the Classic period into Early (A.D. 250-600), Late (A.D. 600-800), and Terminal (A.D. 900-1000) periods. The division between the Early and Late Classic period is made in part by stylistic differences in material culture, as well as significant socio-political changes that include an escalation of warfare and increased competition amongst elites (Stuart 1993).

The Early Classic period was marked by the erection of stelae, widespread use of hieroglyphic writing, and the construction of monumental architecture (Sharer 1994). At the center of this transition, was the formation of kingly dynasties, centered on the divine lord, the *ajaw* (Houston and Stuart 1996). Although the roots of divine kingship lie in the Preclassic period (Freidel, et al. 2002; Freidel and Schele 1988), the institution was fully realized in the Early Classic period. At this time, many Maya sites become truly urban populations and political organization reached state-level complexity (Marcus 1989, 1998, 2004). During the Early Classic period, the great central Mexican site of Teotihuacan exhibited significant influence in the Maya area. However, the nature of this foreign presence is still debated. Some researchers believe Teotihuacan exhibited direct control of select Maya sites (Adams 1986; Coggins 1983). Others see the relationship between Teotihuacan and the Maya as one of mutual trade and respect (Demarest and Foias 1993). Recent hieroglyphic interpretations suggest the relationship was more complex, with the degree of control and influence varying by Maya site (Stuart 2000). Regardless, even after the collapse of Teotihuacan, motifs and images from the great Mexican site remained potent symbols throughout the Late Classic period (Marcus 2003; Stuart 2000: 501).

The Late Classic period marked a climax of sorts for ancient Maya society. The vast majority of the architecture we see at Maya sites today was constructed during this time. Populations grew to their highest levels ever. Estimates for Tikal, one of the largest of all Maya sites, suggest that approximately 62,000 individuals inhabited the site during the Late Classic period (Culbert, et al. 1990). In the Central Zone alone, Turner (1990: 310) estimates a maximum Late Classic population of 2.5 to 3.4 million people. From this figure, Webster (2002: 174) extrapolates that the southern lowlands had a Late Classic population peak of approximately 4.0 to 5.0 million people. At one time, archaeologists believed that the Classic Maya relied on swidden agricultural techniques, much like they do today, and that such methods would not have produced enough food for populations as large as those indicated above. However, survey research since the 1960s has detected a wide variety of surface modifications, such as terracing and raised wetland fields, indicating that the Maya were practicing intensive agriculture techniques throughout the Classic period and may have indeed been capable supporting huge populations (Dunning, et al. 1994; Fedick 1996; Turner and Harrison 1983).

The collapse of Classic Maya civilization is one of the most enigmatic issues in Mesoamerican archaeology. In a matter of one hundred years, from around A.D. 800 to 900, all but a handful of the great Classic period centers were abandoned, with little obvious indication of what became of their former inhabitants (Webster 2002). Traditional models posit that over-exploitation of the land resulted in crop failure which in turn led to disease, starvation, and ultimately the demise of Classic Maya society (Sanders 1973; Santley, et al. 1986).

More recent research, however, has questioned the validity of these models, especially when they are applied to the Maya region as a whole. Critics have documented a diversity of Classic Maya agricultural practices across the region, with sites showing regional adaptation of techniques appropriate to their ecology (Dunning 1996). Not all sites experienced massive

deforestation (Dunning, et al. 1997; Dunning, et al. 1998), and there is no universally documented decline in diet and health (Danforth 1999; Wright and White 1996).

As an alternative to the ecological model for the collapse, or in some cases in conjunction with it, researchers have turned to socio-political explanations. These models center around the failure of the ruling dynasties either as a result of endemic warfare (Demarest 2004; Demarest, et al. 1997), a failure of prestige trade networks (Fahsen and Demarest 2004), or a rejection of the moral authority of divine kingship (Houston, Escobedo, Child, et al. 2003; Sharer and Golden 2004). Regardless, it is unlikely that archaeologists will ever find a single explanation for the collapse—rather it was probably a mosaic event, each area of the Maya lowlands was likely undergoing different processes at the Terminal Classic transition, resulting in a myriad of rapid collapses, slow declines, and, in some cases, fluorescences (Demarest, et al. 2004).

Perhaps the greatest mystery surrounding the Classic collapse is what happened to the thousands of people living in the southern lowlands during the Classic period. In the absence of any evidence for widespread disease and failing health during the Late Classic period (Wright and White 1996), emigration currently stands as the best explanation for the depopulation of the region at the close of the Classic period. Specifically, it has been hypothesized that the Classic-Postclassic transition was marked by major population movements both into rural areas in the southern lowlands and especially to burgeoning Terminal Classic polities in the Yucatán peninsula to the north (Carmean, et al. 2004; Demarest, et al. 2004; Rice and Rice 2004; Ringle, et al. 2004; Suhler, et al. 2004). Although large parts of the Central Zone of the Maya area remained relatively uninhabited until recent years, Maya civilization nonetheless persisted through the Postclassic period and into modern times in the Petén lakes area, Yucatán, Belize, and the highlands.

CLASSIC MAYA POPULATION HISTORY

In the section that follows, I provide a more detailed archaeological background for each of the archaeological zones in the southern half of the Maya area, the focus of this study (Figure 2.1). This division of the Maya area into archaeological zones first appeared in *The Classic Maya Collapse* (Culbert 1973a) and the version used here is modified from *Precolumbian Population History* (Culbert, et al. 1990). The division between these archaeological zones is based in part on regional variability in material culture, but also on differences in culture history. Though these archaeological zones do not correspond to any emic socio-political organization recognized by the ancient Maya, the history and development of sites within each zone were more closely intertwined with one another than they were to sites beyond each zone. The division of the Maya area into archaeological zones remains a useful organizational tool in Maya archaeology (e.g. Rice and Forsyth 2004). In this discussion, I highlight some of the key characteristics of each archaeological zone.

In formulating this review, I emphasize areas of the archaeological record important for reconstructing population history. Here, I use population history as a broad-reaching term that incorporates the origins, development and decline of Maya populations. In this review, I discuss the Preclassic roots of settlement in each zone and the growth and subsequent decline of the major Classic period sites. I emphasize historical events that may have resulted in major population changes during the Classic period. Absent from this review is any discussion of population genetics even though it is one of the most useful tools for reconstructing human population history (Relethford 2003). To date, biological studies of Maya population history are largely lacking and I have reserved a discussion of this research for Chapter IV.

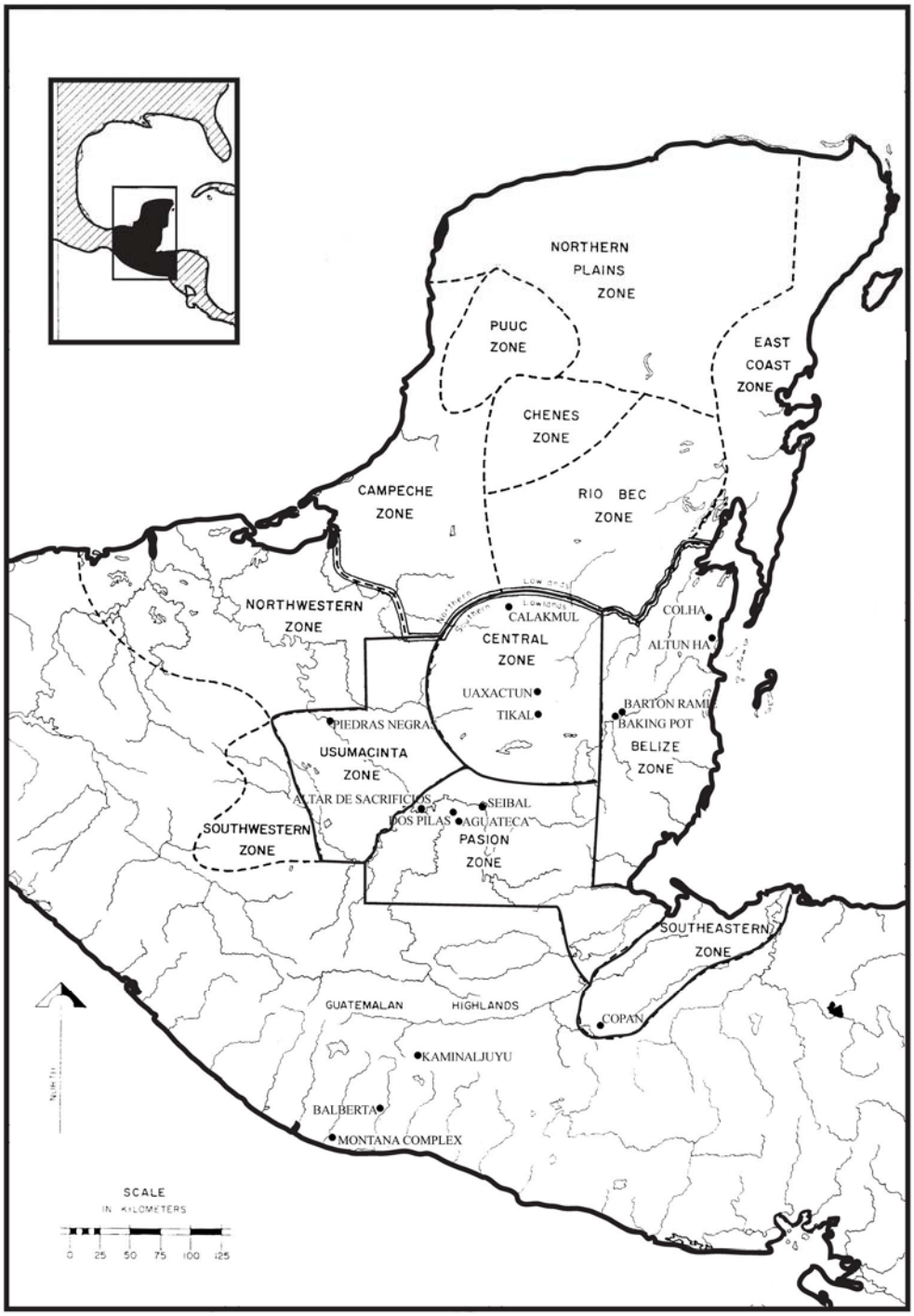

Figure 2.1. Map of the Maya area featuring sites with skeletal samples used in this study (modified from Culbert and Rice 1990: 29).

Central Zone

The Central Zone is generally considered the heartland of Maya civilization. Located in Department of Petén, Guatemala, as well as portions of southern Mexico and western Belize, the Central Zone is the seat of some of the largest and most significant Maya sites, notably the superpower sites of Tikal and Calakmul. In addition, the impressive Late Preclassic centers of El Mirador and Nakbe arose in the Central Zone. These sites possess some of the earliest, not to mention the largest, ancient Maya monumental architecture (Hansen 2001, 2004). Mysteriously, the greatest Preclassic sites of the Central Petén did not survive into the Classic period. Hansen (2001) speculates that endemic warfare may in part be responsible for the Preclassic collapse of El Mirador and Nakbe.

However, not all of the Preclassic centers of the Central Zone collapsed. Major sites such as Tikal, Uaxactun, and Calakmul all have their roots in the Preclassic period and continued on into the Classic period. By the Late Preclassic period, Tikal was becoming a significant power in the region. The earliest monumental construction at Tikal, found in the North Acropolis and the Mundo Perdido complex, dates to the end of the Middle Preclassic period (Laporte and Fialko 1995). By the Late Preclassic – Early Classic transition (sometimes known as the Protoclassic) the population of Tikal was growing rapidly (Harrison 1999: 64). Tikal's neighbor, Uaxactun, as well as the site of Calakmul, began to grow in prominence. The Early Classic period growth of Tikal, Calakmul, and Uaxactun may in part have been fueled by the collapse of El Mirador, Nakbe, and other Late Preclassic sites.

By the Early Classic period, Tikal, Uaxactun, and Calakmul were all sites of relative significance within the Central Zone. At this time, Calakmul and Uaxactun were allied with one another against their rival Tikal (Carrasco 1998). During the first part of the Early Classic period, all three sites were roughly the same size (though the Early Classic period is poorly

known at Calakmul). However, this all changed in A.D. 378 with the arrival of Siyaj K'ak', presumably an emissary from the Central Mexican site of Teotihuacan (Stuart 2000). He is identified in both the inscriptions of Tikal and Uaxactun. Whatever the exact nature or purpose of his appearance, from henceforth Uaxactun lived in the shadow of Tikal, which transformed itself into one of the great Maya superpowers (Martin and Grube 2000: 30).

By the close of the Early Classic period, Tikal and Calakmul established themselves as dominant powers, not just in the Central Zone, but throughout the Maya area. Compared to other sites, Tikal and Calakmul possess a large number of Early Classic stelae; unfortunately the monuments of Calakmul are badly eroded and difficult to read (Martin and Grube 2000: 101). During the Early Classic period, other sites began to mention Tikal and Calakmul in their inscriptions—providing further evidence of the extensive alliance building occurring at that time. By the Late Classic period, Tikal and Calakmul grew into full-fledged enemies, drawing much of the Maya world into their conflict (Martin and Grube 1995).

There is little question that Calakmul and Tikal were the largest Maya sites during the Classic period. Calakmul boasted a population of approximately 50,000 individuals (Folan, et al. 1995) and Tikal was home to around 62,000 inhabitants (Culbert, et al. 1990). No doubt these large populations were a result, in part, of natural growth of earlier, Preclassic populations at each site. However, Fry (1990) identified a substantial increase in the Early Classic population at Tikal, relative to Preclassic times, which likely is the result of immigration into the site. Thus, population aggregation, in addition to natural growth, explains the large size of these superpowers. It is possible that these immigrants were from local sites in the area, from the abandoned Preclassic superpowers, or from sites outside the region.

Tracing migration during the Classic period is delicate a matter, however. The hieroglyphic record indicates an abundance of events in which emissaries of Tikal and Calakmul

visited other Maya sites and vice versa (Martin and Grube 2000). Of particular note, are cases of royal marriage where daughters of one site were sent to be married into the dynasty of another. In these instances, we have documented evidence for gene flow into and out of Tikal and Calakmul. Another tantalizing line of evidence comes from the analysis of oxygen and strontium stable isotopes of human bone and teeth, which has demonstrated the presence of a number of nonlocal immigrants in both elite and nonelite contexts at Tikal (Wright 2004a). Taken together, these data indicate some level of gene flow into Tikal and Calakmul from not only outside the site, but beyond the Central Zone.

Nonetheless, there is a strong local tradition of art, architecture, and ceramic styles at Central Zone sites that points to strong regional continuity for the populations of the area. For instance, the major pyramids of Calakmul, Tikal, and Uaxactun all prominently featured massive stucco masks—a tradition that can be traced back to Preclassic El Mirador (Carrasco 1998: 374). Similarly, the ceramics of Uaxactun, Tikal, and Calakmul are all remarkably similar. Even at the height of their conflict, Late Classic ceramics at Calakmul and Tikal resemble one another (Rice and Forsyth 2004: 36). Although material culture does not directly equate with genes, the data show no evidence of a major population movement into the Central Zone from elsewhere during the Classic period.

Despite the strength of Calakmul and Tikal, these sites fell into ruin during the ninth century, as did most of the Central Zone. The processes underlying the collapse of these sites remain debated. Valdés and Fahsen (2004) favor a scenario in which escalating violence and erosion of elite rulership led to the demise of Tikal. Based on fluctuations in the annual discharge of the Río Candelaria, Braswell and colleagues (2004) propose that the fall of Calakmul may have been due to the combined affects of environmental degradation, climate

change, all in combination with Calakmul's weakened political state after its defeat by Tikal in A.D. 699.

Usumacinta Zone

The Usumacinta Zone was dominated by the sites of Tonina, Palenque, Piedras Negras, and Yaxchilan, the latter two of which were locked in a bitter conflict throughout much of the Classic period. The Preclassic and even the Early Classic periods are obscure in the Usumacinta Zone. Although only Piedras Negras has been extensively excavated, the current data from the Usumacinta Zone indicates that sites in the area remained small until the latter half of the Early Classic period (Houston, Escobedo, Child, et al. 2003). As slow as the Usumacinta sites were to develop, they were also the first to fall into decline around A.D. 800. The notable exception is Tonina, which boasts the latest Long Count date in the southern Maya lowlands at A.D. 909 (Martin and Grube 2000: 177).

As with the Central Zone, there is a strong tradition of art, architecture, and artifact styles that is relatively unique to the Usumacinta Zone. In the Usumacinta Zone, the vertical pyramids common to the Central Zone were rarely constructed. This was especially true in the Late Classic period. Rather, the architects of the Usumacinta emphasized the natural landscape, placing large vaulted range structures atop tall hills to achieve the same sense of verticality. Nonetheless, some true pyramids are present in the Usumacinta area, though they are relatively low, with an emphasis on the superstructure. The best examples are the Temple Inscriptions at Palenque and Structure O-13 of Piedras Negras (Macri 1994).

The Late Classic period ceramic tradition of the Usumacinta Zone is generally distinct from that of the Central Zone (Rice and Forsyth 2004). Elaborate polychrome ceramic wares, especially codex-style vases, which are characteristic of the Central Zone, are notably rare in the

Usumacinta Zone. However, when Piedras Negras is compared with its frontier settlements and even with border sites in the enemy Yaxchilan kingdom, the ceramics are similar, particularly during the latter part of the Late Classic period (Golden, et al. 2004). These stylistic differences suggest a local development of Usumacinta Zone ceramics with little to no influence from outside the area.

The stylistic distinctiveness of the art, architecture and artifact styles of the Usumacinta Zone is suggestive of a degree of isolation from other parts of the Maya world. Transportation between sites of the zone would have been relatively easy by way of the Usumacinta River and adjacent valleys (Anaya 2001). However, the Sierra del Lacandón mountain range served as a formidable barrier, separating the western Maya area from the rest of the Maya world. All of this raises the question, how isolated were populations of the Usumacinta Zone from other areas of the Maya lowlands?

Of all the sites in the Usumacinta Zone, archaeological data is strongest for the site of Piedras Negras, due to extensive archaeological explorations by the University of Pennsylvania in the 1930s (Mason 1933; Satterthwaite 1933, 1936, 1938) and Brigham Young University-Universidad del Valle in the 1990s (Escobedo and Houston 1997, 1998, 1999, 2001). During the Preclassic period and the first part of the Early Classic period, the site was little more than a small village (Houston, et al. 2003). However, around A.D. 400-450, Piedras Negras underwent a population explosion, inferred from a boom in construction around the site that continued into the Late Classic period. It is likely that this population expansion was partly due to immigration into the site. Houston and colleagues (2003) tentatively suggest that at least some part of this immigrant population originated in the Central Petén. However, recent archaeological work in the area by my colleagues and I on the Sierra del Lacandón Regional Archaeological Project have found that a number of settlements in the Piedras Negras area have extensive Preclassic and

Terminal Classic settlement, but lack any major Classic period—especially Late Classic—component (Golden, et al. 2004). This indicates to us a model in which primate centers of the Usumacinta Zone, such as Piedras Negras, literally absorbed people off the countryside at the height of their power during the Late Classic period. Thus, we suspect that the major population explosion at Piedras Negras—and likely the other major sites in the Usumacinta Zone—was largely due to local, rural immigration, not immigration from other parts of the Maya area.

Pasión Zone

The sites of the Pasión Zone are situated in proximity to the Pasión River, a major tributary of the Usumacinta River. The important Classic period sites include Altar de Sacrificios, Seibal, Dos Pilas, Arroyo de Piedras, Tamarindito, Aguateca, and Punta de Chimino. The Pasión Zone benefits from being one of the most thoroughly investigated regions in the Maya area, from both an archaeological and epigraphic perspective.

Settlement in the Pasión zone stretches back into the Middle Preclassic period. At Altar de Sacrificios and Seibal, the Peabody Museum uncovered evidence of Middle Preclassic occupation dating to about 900 to 500 B.C. (Willey 1973a, 1990). By the Late Preclassic period, both Seibal and Altar de Sacrificios exhibited the roots of Classic society, including the presence of major ceremonial architecture and the aggregation of substantial populations. At Seibal, population levels rose substantially throughout the Late Preclassic period, such that by the end of the period as many as 5,000 to 10,000 people inhabited the site (Willey 1990).

In the Petexbatun area, Late Preclassic ceramics have been identified (Demarest 1997; Foias 1996). Settlement in the region appears to have been focused along Lake Petexbatun and its associated riverways, with Punta de Chimino, Aguateca, Tamarindito, and other sites all exhibiting evidence of Late Preclassic ceremonial architecture (Demarest 1997: 218). The one

notable exception to early occupation in the Petexbatun region is the site of Dos Pilas, which appears to have been settled only in the Late Classic period, though Early Classic ceramics were found in nearby caves.

In the Early Classic period, sites of the Pasión region developed all of the hallmarks of Classic Maya society. Altar de Sacrificios exhibited a fully developed Early Classic tradition, including a number of stelae, polychrome pottery, and numerous ceremonial structures that served as the foundation for Late Classic constructions (Willey 1973a). In contrast, Seibal appears to have faltered during the Early Classic period (Willey 1990). Evidence for polychrome pottery is lacking at the site and some Late Preclassic compounds appear to have been abandoned during this time period. In the Petexbatun region, Tamarindito was the dominant power during the Early Classic period (Demarest 1997; Martin and Grube 2000). During this time, Tamarindito constructed numerous ceremonial structures and may have maintained some degree of political dominance over Arroyo de Piedra, the only other Early Classic polity in the Petexbatun region (Escobedo 1997; Valdés 1997).

All of the sites of the Pasión region that stumbled in the Early Classic period, including Seibal, thrived during the Late Classic period. The Late Classic revitalization of Seibal is hypothesized to have been in part due to the immigration of populations from other nearby Pasión sites (Willey 1990: 248). Undoubtedly, the dominant power in the Pasión region during the Late Classic period was the site of Dos Pilas. Unlike its neighbors, there is little evidence for a population at Dos Pilas prior to the Late Classic period. Rather, the site was founded by a splinter lineage of the Tikal dynasty, with which Dos Pilas shares its emblem glyph. Previous interpretations of the hieroglyphic record suggested that the founders of Dos Pilas were exiles from Tikal, either a rebellious faction of the royal family or an ousted king and his retainers (Houston 1993; Martin and Grube 2000; Matthews and Willey 1991). However, recently

uncovered portions of Dos Pilas' hieroglyphic stairway suggest a slightly different story (Fahsen 2003). It is now clear that the founder of Dos Pilas, Balaj Chan K'awiil, was a brother of the Tikal king Nuun Ujol Chaak. In its early days, Dos Pilas was an ally of Tikal, presumably founded to serve its interests in the Pasión region. However, around A.D. 650 Dos Pilas was sacked by Calakmul. Rather than being sacrificed, the Dos Pilas king was forced to swear loyalty to the Calakmul king and henceforth fought as an ally of Calakmul against Tikal. From that point forward, Dos Pilas, with the support of Calakmul, consolidated its power and became the dominant power in the Pasión region. Eventually, Dos Pilas subjugated the entire Petexbatun region, including Arroyo de Piedras, Tamarindito, and Seibal (Demarest 1997: 218).

At the height of its power, Dos Pilas was home to some 2,000 to 4,000 individuals (Palka 1997). Although it is clear that the royal family of Dos Pilas emigrated from Tikal, the origin of the rest of the population is less clear. During the Late Classic period, the ceramics of the Petexbatun region are markedly uniform, suggesting a local origin for the Dos Pilas population (Foias and Bishop 1997). Settlement at Dos Pilas is also similar to neighboring Pasión sites, with **C**-shaped structures frequently found at Seibal and Dos Pilas but relatively uncommon elsewhere in the southern lowlands (Houston 1993: 52). The homogeneity in ceramic and architectural styles suggests a local origin for the Dos Pilas population; though it is possible that these traditions could have been adopted by immigrants.

Dos Pilas' control over the region lasted only a century. Beginning around A.D. 760, Dos Pilas and other sites in the region show evidence of decline, including cessation of monumental construction and depopulation (Demarest 1997). The Vanderbilt Regional Petexbatun Project has identified a series of defensive structures at Dos Pilas and other sites in the region that appear to have been erected around this time (Demarest, et al. 1997). Evidence indicates the entire region erupted into violent conflict from which it never recovered, leading to

its complete collapse by A.D. 830. The destructive nature of this conflict is best demonstrated at the small center of Aguateca, which served as the seat of the local dynasty after the destruction of Dos Pilas (Inomata 1997). At Aguateca, numerous structures show evidence of burning and hasty abandonment.

The only sites of the region to survive this cataclysm were Seibal, Altar de Sacrificios and Punta de Chimino, with Seibal probably dominating the area. Around A.D. 830, new ceramic types and an iconographic style reminiscent of Central Mexico were introduced to Seibal (Tourtellot and González 2004). Traditionally, these changes were cited as evidence of an intrusion, possibly violent, of a Mexicanized group of Maya from the Putun region of the Gulf coast of Tabasco, Mexico (Sabloff and Willey 1967; Sabloff 1973; Willey 1973b). However, recent hieroglyphic interpretations suggest Seibal was revitalized by the refounding of its dynasty by a representative of the site of Ucanal to the east (Schele and Matthews 1998: 179). However, by the early tenth century Seibal, like its contemporaries, was in ruin.

Belize Zone

Ironically, Belize is perhaps the most thoroughly excavated area of the Maya lowlands, yet remains relatively enigmatic. In total contrast to the Usumacinta Zone, it has provided some of the best evidence for both Preclassic and Postclassic settlement in the southern lowlands, yet the art and architecture of the Belize area is relatively simple, and hieroglyphic writing is rare compared to sites to the west. Due to the diversity of sites in the Belize Zone, it is difficult to present a generalized population history for this part of the Maya area.

Preclassic settlements were scattered throughout Belize, at sites like Lamanai (Pendergast 1981), Cuello (Hammond 1991a), Cerros (Freidel, et al. 1982), and Colha (Hester and Shafer 1994), although none of the Belizean sites matched the size of Central Zone centers

like El Mirador and Nakbe. Like the Central Zone, some sites in Belize were abandoned at the end of the Late Preclassic period while others went on to fluoresce during the Classic period.

In the Classic period, sites situated in the western part of the Belize Zone, such as Xunantunich and Caracol, were closely tied to sites in the Central Zone. These sites demonstrated dramatic population growth during the Classic period and at Xunantunich there is evidence that the site attracted immigrants from surrounding populations (Ashmore, et al. 2004). Other sites, like Barton Ramie, demonstrated relatively consistent populations throughout the Classic period (Fry 1990).

Unlike other parts of the southern Maya lowlands, there was a mosaic collapse in the Belize Zone—some sites were abandoned during the Terminal Classic period while others persisted into the Postclassic period. The collapse of Xunantunich resulted in the abandonment of both the site center and the surrounding hinterland (Ashmore, et al. 2004). Caracol maintained a veneer of strength until the end of the Terminal Classic period, though internal fragmentation is apparent for most of the ninth century (Chase and Chase 2004). Similarly, Altun Ha collapsed in the ninth century. In contrast, Lamanai and other sites in northern Belize apparently survived the collapse by re-orienting themselves to emerging economies and political developments in the Yucatán (Masson and Mock 2004; Pendergast 1986). In other cases, sites like Colha were abandoned during the ninth century A.D., only to be re-occupied a century later during the Postclassic period (Hester and Shafer 1994). Overall, while some major sites in Belize demonstrated the seesaw pattern of demographic explosion and collapse typical in the Central Zone, Fry (1990) found that the minor Belizean centers of Barton Ramie and Pulltrouser Swamp were not subject to the same demographic swings. Barton Ramie's population proved stable throughout the Classic period and lasted into the Early Postclassic period.

As a result of the relative absence of stelae and hieroglyphic texts, the Belize Zone has been viewed as a peripheral zone, even a backwater, by Maya archaeologists (Hammond 1981). The relative distinctiveness and diversity of Belizean ceramics underscores the uniqueness of this area (Rice and Forsyth 2004). Nonetheless, the Belizean Zone was more than a rural hinterland. For instance, at Altun Ha there is clear evidence of at least some form of interaction with the Central Mexican site of Teotihuacan (Pendergast 2003). Similarly, lithic tools made from materials from the northern Belize Chert Bearing Zone and presumably produced in the Colha workshops were traded as far inland Tikal (Hester, et al. 1994: 59). Further, the ceramics of the Colha region demonstrate a strong affinity for the Central Petén, as opposed to neighboring Belizean sites (Rice and Forsyth 2004; Valdez 1987). Thus, although Belizean sites never achieved the same level of population size or artistic achievement as sites in other regions, by variably allying themselves with waxing and waning powers throughout Precolumbian times they proved to be some of the most persistent of all Maya communities (Masson and Mock 2004).

Southeastern Zone

In many respects, the Southeastern Zone is a peripheral zone in the Maya region. Located in southeastern Guatemala and western Guatemala, the region is home to the large Maya centers of Quirigua and Copan. This part of the Maya region is somewhat enigmatic in that it is quite clearly part of the Classic Maya tradition, yet it exhibits both environmental and cultural traits that set it apart from its counterparts to the north—particularly its early affinity to sites in the Guatemalan highlands and Pacific Coast (Fash 2001; Valdés and Wright 2004). Although both the architecture of Copan and Quirigua are relatively modest compared to other major Maya sites, the sculptural program is among the most well-executed and ornate in the Maya world.

Of the sites in the Southeastern Zone, Copan is undoubtedly the best studied. Copan was settled during Preclassic times. During this time period, the site was relatively insignificant, with modest architecture. Copan remained small during the first part of the Early Classic period. For many years, the first Maya Long Count date known to archaeologists for Copan was A.D. 485. This led scholars to believe that this date marked the introduction of Maya culture to what was originally a non-Maya site (Morley 1920). However, Fash and Stuart (1991) believe that the archaeological evidence points to a strong affinity between Copan, the Guatemalan Highlands, and the Pacific Coast during the Preclassic period and the first part of the Early Classic period. They argue the earliest inhabitants of Copan were Ch'olan Maya and that it was from this indigenous base that Classic Maya society at Copan developed. Similarly, Valdés and Wright (2004) suggest that a strong relationship with the highland site of Kaminaljuyu nurtured early development at Copan, and raise the possibility that Ch'olan migrants departing Kaminaljuyu at the end of the Late Preclassic period settled there.

Recent hieroglyphic readings have identified Yax K'uk Mo' as the founder of the Copan dynasty in A.D. 426 (Stuart 2004). Iconographic data (Stuart 2004), archaeological evidence from the tomb attributed to him (Bell, et al. 2004), and the stable isotope analysis of his purported skeletal remains (Buikstra, et al. 2004) all indicate that Yax K'uk Mo' was a foreigner, most likely from somewhere in the Central Petén, who had ties to both Tikal and the Central Mexican site of Teotihuacan.

Under the rule of Yax K'uk Mo' and his royal descendants, Copan grew into one of the largest and most powerful ancient Maya polities. The kingdom consisted of both Copan proper, known to archaeologists as the Copan pocket, as well as outlying settlement within the Copan valley (Fash 2001: 165). Archaeological work beyond the Copan pocket has identified a series of secondary sites, subordinate to the lords of Copan. Prior to the rise of the Copan dynasty in

the 5th and 6th centuries, these communities were only loosely affiliated with Copan (Canuto 2004). However, by the Late Classic period they were fully incorporated into the Copan kingdom. Settlement at Copan boomed during the Late Classic period, particularly within the Copan pocket. Webster and Freter (1990: 56) estimate a population of 18,000 to 20,000 individuals for the entire Copan polity.

By the Late Classic period, the power of Copan extended beyond the Copan Valley, to subordinate the kingdom of Quirigua. Quirigua remained a relatively modest site until the latter years of the Early Classic period (Sharer 1991). By the Late Classic period, Quirigua was a site of some importance when it fell under the Copan hegemony (Fash and Stuart 1991). However, in A.D. 738 K'ak' Tiliw Chan Yoatt, king of Quirigua, captured and executed Waxaklajuun Ub'aah K'awil, king of Copan (Martin and Grube 2000: 205). From that point forward, Quirigua entered its most glorious years while Copan entered a slump from which it never fully recovered. The royal dynasties of both Copan and Quirigua collapsed in the early part of the ninth century. Fash and colleagues argue that the roots of Copan's demise lay in the faltering of the dynasty at the expense of increasing non-royal elite competition, perhaps exacerbated by degraded environmental conditions within the valley (Fash, et al. 2004). Webster, Freter, and Storey contend, based on obsidian hydration dating, that the non-elite abandonment was a slow process, with major occupation in the valley lasting until the thirteenth or fourteenth century A.D (Webster and Freter 1990; Webster, et al. 2004). However, Fash, Andrews, and Manahan (2004) argue that the majority of the Copan valley was abandoned following the demise of the dynasty. They point out that the reliability of obsidian hydration dating is questionable (Braswell 1992) and that Manahan (2004) has identified an early Postclassic occupation at Copan, which is both ephemeral and appears to consist of new migrants to the valley.

Highland Guatemala

Our knowledge of the Highlands during the Preclassic and Classic periods comes almost entirely from the site Kaminaljuyu. As early as the Middle Preclassic period, Kaminaljuyu demonstrated evidence of social complexity (Valdés and Wright 2004). By the Late Preclassic period, Kaminaljuyu was one of the dominant powers in the Maya area, serving as a central node of trade between the highlands, the Pacific coast, and the lowlands (Popenoe de Hatch 2002). The success of Preclassic Kaminaljuyu was due in part to its location on the fertile soil of the Valley of Guatemala and its elaborate irrigation canal system (Popenoe de Hatch 2002). Some of the earliest evidence of hieroglyphic writing in the Maya area comes from the monumental sculpture of Kaminaljuyu's Late Preclassic period (Kaplan 2002). Epigraphic evidence suggests the Preclassic inhabitants of Kaminaljuyu were Ch'olan speakers (Fahsen 1999).

At the close of the Preclassic period, Kaminaljuyu fell into a decline that eventually led to a massive exodus of people from the site. Shook and Popenoe de Hatch (1999) believe that this event may in part have been due to failure of the canal irrigation system at Kaminaljuyu as well as pressure from invading groups from the west. The former inhabitants of Kaminaljuyu may have migrated east into the Motagua valley, toward Copan, where other Ch'olan populations were already located (Valdés and Wright 2004). Kaminaljuyu recovered from this loss in the Early Classic period and the site continued to grow to its largest size in the Late Classic period (Michels 1979c). Based on ceramic evidence, Popenoe de Hatch suggests the Early Classic revitalization of Kaminaljuyu can be attributed to re-settlement by a new population—Maya from the western Highlands—though a remnant population from earlier times still remained (Popenoe de Hatch 2002).

The Early Classic period is an intriguing time at Kaminaljuyu. During this time, the practice of erecting carved monuments had ceased, indicating a fundamental shift in the socio-

political structure of the site (Popenoe de Hatch 2002). Early Classic Kaminaljuyu demonstrates architectural and artifactual affiliations with the Central Mexican site of Teotihuacan (Valdés and Wright 2004). Although earlier researchers saw this as evidence of Teotihuacan's dominance over Kaminaljuyu (Kidder, et al. 1946), today researchers more commonly believe the connection was one of trade and mutual interaction (Braswell 2003; Demarest and Foias 1993). In fact, the presence of Teotihuacan features at select Early Classic Maya sites—Kaminaljuyu, Tikal, and Copan—may be more telling about the nature of interaction between these sites, than it is of any connection with Central Mexico (Valdés and Wright 2004).

By the Late Classic period, Kaminaljuyu was a major center in terms of population size, though it was nonetheless overshadowed by its contemporaries in the lowlands in regards to material culture and artistic achievements (Popenoe de Hatch 2001). Based on the presence of eleven ballcourts, Popenoe de Hatch (2002) speculates that, by the Late Classic period, Kaminaljuyu was suffering from political decentralization and social competition amongst the ruling elite. These processes may have contributed to the collapse of Kaminaljuyu, though direct evidence of the site's demise remains elusive.

Pacific Coast

The Pacific Coast of Guatemala and Chiapas is one of the least understood regions of the Maya area (Bove 1989a). This lack of knowledge can be attributed to an archaeological emphasis on the lowlands, the seat of Classic Maya civilization. Nonetheless, the Pacific Coast was integral to the development of complex society in the Maya area during the Preclassic period and supported large sites throughout prehistory. Sites on the Pacific Coast demonstrate complex interactions with many parts of Mesoamerica—the highlands, the Maya lowlands, the Mexican Gulf Coast, and Central Mexico. Adding to the enigma, it is not clear if the inhabitants

of this region were of a Mayan language group or if other ethnicities were present during Precolumbian times (Bove 1989b).

In the Middle Preclassic period, some of the earliest Mesoamerican sites with evidence for social complexity are found on the Pacific Coast (Blake, et al. 1995; Clarke and Blake 1994). Similarities in sculptural styles from this time period, link the Pacific Coast to sites in Chiapas and the Gulf Coast Olmec area, indicating a rich network of interaction and exchange (Popenoe de Hatch 1989). Researchers currently theorize that these early populations spoke a Mixe-Zoquean language (Gasco 2001; Lowe 1977). By the Late Preclassic period a number of sizable sites developed on the Pacific Coast, including Abaj Takalik and Balberta. Abaj Takalik exhibits some of the earliest Maya hieroglyphic writing (Bove 2001). The close of the Preclassic period on the Pacific Coast was a period of disruption, with many older sites abandoned and new sites founded (Bove 1989b).

During the Early Classic period, the site of Balberta was among the largest and most influential centers along the Pacific Coast, having dominion over smaller centers in the region (Bove and Medrano 2003). Balberta demonstrates a strong connection to the Central Mexican site of Teotihuacan during this time period. There is some debate over whether this connection represents mutual trade between the two or an actual Teotihuacano military incursion into the region. However, Bove and Medrano (2003) cogently argue that there is a lack of any real Teotihuacano colony at Balberta, which would be observable in the presence of domestically made Central Mexican style artifacts. Rather, they suggest the relationship was one of a mutual interaction of peers. Balberta was rapidly abandoned at the close of the Early Classic period (Bove and Medrano 2003).

Another prominent Pacific Coast center is the Montana site complex (Bove and Medrano 2003). During the Early Classic period, Montana was a sizable center though was not a

significant player in the politics of the region. However, in the beginning of the Late Classic period it joined with the nearby settlement groups of Manantíal, Loma Linda, and Paraíso to become a dominant Pacific Coast center (Bove and Medrano 2003). In contrast to Balberta, there is substantial evidence of a Teotihuacan colonization of the Montana complex in the form of locally-made Teotihuacan-style artifacts. Bove and colleagues (2003) argue that the rapid rise of the Montana complex, coupled with the dramatic collapse of Balberta at the Early Classic – Late Classic transition, is a direct reflection of a major Teotihuacano colonization event, and possible military incursion into the region. As with the lowland area, the majority of major sites on the Pacific Coast were abandoned at the close of the Classic period, the reasons for which are still unknown (Bove 1989b).

SUMMARY

This first part of this chapter provided a brief overview of the ancient Maya, discussing the regional distribution of Maya sites and providing a Preclassic and Classic period archaeological chronology. The second part of this chapter included a more detailed discussion of each archaeological zone, focusing on information pertaining to population history. This review will be used to generate research hypotheses in the following chapter.

CHAPTER III

BIOLOGICAL MODELS AND RESEARCH HYPOTHESES

As discussed in the previous chapter, the majority of our current data on ancient Maya population history is archaeological. In this chapter, I use this archaeological background to formulate research hypotheses that can be tested with biological data and models for ancient Maya population history. First, I provide an overview of the assumptions and caveats of using skeletal samples to reconstruct ancient population parameters. I then justify why I expect that ancient Maya skeletal samples will serve as realistic representations of ancient populations. In the second portion of this chapter, I develop the research hypotheses to be tested by this study. In my research hypotheses, I first establish the validity of the methodological approach, then I consider the nature of ancient Maya population structure, and last, I use the results of my analyses to test questions pertaining to ancient Maya population history.

BIOLOGICAL ASSUMPTIONS

One of the greatest obstacles in bioarchaeological research is the extrapolation of biological parameters derived from studies of living populations to the analysis of ancient skeletal collections. Since the goal of bioarchaeology is to answer biocultural questions about ancient societies, one of its hallmarks is the analysis of human remains at the level of the population, as opposed to research on a single skeleton or a handful of skeletons (Buikstra 1977; Larsen 1997). Rather, bioarchaeologists study large collections of skeletons that are believed to be representative of ancient populations in terms of biological parameters pertaining to demography, diet, health, genetics, etc. However, skeletal samples are not the same as living populations, although bioarchaeologists often treat them as if they are. Thus, in any

bioarchaeological study it is necessary to consider the ways in which skeletal samples are representative of ancient populations, and how they differ (Wood, et al. 1992).

In this dissertation, I use skeletal samples to represent ancient human populations in order to study Classic Maya population structure and history. This approach is more popularly known as the analysis of "biological distance" in the anthropological literature (Buikstra, et al. 1990). In biological distance studies, bioarchaeologists use phenotypic characters of the skeleton to reconstruct population history, in much the same way that population geneticists use genetic markers. In both approaches, one must assume that the study sample is representative of the greater population. In population genetics, a population is defined as (1) a group of individuals of the same species, (2) living in the same geographic area, and (3) where any one member of the group has the potential to breed with any other member of the group (Hartl and Clark 1997: 71).

In bioarchaeological studies, this definition is often only partly met. The first criterion is not a problem—bioarchaeology only focuses on ancient anatomically modern *Homo sapiens* populations. Generally, we can also make the case that our skeletal samples are comprised of individuals from the same geographic area. For instance, we assume that all of the individuals interred in a cemetery, burial mound, etc. come from the same community or a series of interbreeding communities (village, band, city, etc.). However, in some biological distance studies, researchers use pooled individuals from different sites, due to poor sample sizes, into larger samples for analysis. In such instances, individuals from different populations may become aggregated. This is especially common in studies of biological variability across large regions, such as research on the peopling of the New World (e.g. Jantz and Owsley 2001; Powell and Neves 1999; Steele and Powell 1999; Turner 1985a, 1986).

It is the last component of the population definition that is the most problematic—that any member of the group has the potential to breed with any other member of the group.

Because burial samples are often multi-generational, spanning decades to centuries, not all of the individuals in a skeletal sample would have been able to interbreed. In studies that focus on a limited archaeological region, as opposed to inter-regional or global studies, researchers are generally able to rely on skeletal samples that at the most span a few hundred years (e.g. Corruccini and Shimada 2002; Howell and Kintigh 1996; Konigsberg and Ousley 1995; Rhoads 2002; Stojanowski 2001). Thus, although bioarchaeologists almost invariably work with multigenerational skeletal samples, their analyses are strongest when the overall period of time covered is limited to decades or at the most hundreds of years.

Ultimately, bioarchaeologists, including those working in biological distance, must use skeletal samples as proxies for true biological populations. The validity of any bioarchaeological study is dependent on how realistically the skeletal samples serve as substitutes for true populations. For instance, numerous researchers have justly criticized Turner's study of New World dental variation on the grounds that he pooled samples from across the Americas, which spanned the entire human settlement of the hemisphere, to create artificial samples with very little grounding in biological reality (Campbell 1986; Meltzer 1993; Powell 1993, 1995). In this example, Turner violated both the requirement that members of a population share a geographic space and that they be capable of interbreeding, or at least be within a limited number of generations. Although Turner does not make the claim that his samples represent true populations, he nonetheless offers interpretations of his results that imply that his samples behave as populations in an evolutionary sense.

In the present study, I incorporated skeletal samples that were close proximates to actual biological populations. Each sample in my analysis represents the Classic period settlement of a single Maya site. Fortunately, the ancient Maya buried their dead either beneath their houses or in nearby funerary monuments (McAnany 1995). In this regard, we can assume with reasonable

certainty that the Maya interred their dead in the community in which they lived. When foreigners are identified in Maya burial samples, they are most commonly identified as individuals who migrated to the site and took up residence and joined the breeding population, though in some cases these foreigners may have been victims of battle (Buikstra, et al. 2004; Valdés and Wright 2004; Christine D. White, et al. 2001; Wright 2001). Therefore, I treat each archaeological site as a population with a finite geographic limit. Only in the case of the Pacific Coast sample—where two nearby sites were combined to make a single sample—do I consciously violate this requirement (see Chapter V). Second, I have restricted the temporal range of the samples I use in this analysis. With the exception of about 10 individuals from the Pacific Coast, all of the skeletons are from the Classic period, and the majority of the individuals dating to the Late and Terminal Classic periods. Although this is a sizable span of time, it is more conservative than is used in many regional biological distance studies (Irish 1993; Powell 1995; Sutter 1997). In contrast to other biological distance studies that compare samples from different time periods (e.g Haydenblit 1996; Konigsberg 1990b; Stojanowski 2004), this research compares only contemporaneous samples, thereby eliminating the possible role that temporal genetic drift or selection may have played in biological variability in the Maya area.

RESEARCH HYPOTHESES

In Chapter II, I described our current understanding of Classic Maya population history, summarized by archaeological zone. From this summary, it is clear that each archaeological zone has a unique history while playing a part in the greater Classic Maya tradition. On one hand, the distinctiveness of each zone would suggest relative isolation for the populations of each zone. Yet, the archaeological and hieroglyphic record contain evidence for major population movements throughout the Classic period.

To better understand Classic Maya population history, I will use phenotypic aspects of the skeleton, specifically dental metric and nonmetric traits. I focus my analysis on the Classic period since it is the time period that is most thoroughly understood, and contains the largest sample sizes. However, before I begin to explore questions relating to ancient Maya population history, I must determine whether the methodology I have chosen is a valid tool.

Hypothesis #1: Classic Maya populations exhibit among-group genetic variabilty and this variability can be meaningfully measured by phenotypic differences in dental nonmetric and metric data.

Previous research has demonstrated that dental metric and nonmetric data are useful tools for reconstructing ancient biological variability (Kieser 1990; Scott and Turner 1997). Nonetheless, I must establish whether these phenotypes vary in any significant manner between the ancient Maya skeletal samples in question. Thus, I will perform multivariate analyses of biological variability between Maya sites using dental nonmetric and metric data. Hypothesis #1 will be validated if the biological distance values derived from either the dental metric or nonmetric analyses, or both, are statistically significant. Ideally, each dataset should independently produce similar results. If the results are dissimilar, I must determine what factors may explain the differences.

If Hypothesis #1 is valid, I will use dental metric and nonmetric data to explore biological variability and population history for the Classic Maya. If Maya populations are phenotypically different from one another, what processes underlie those differences? In the absence of gene flow, I expect Maya population structure will follow an isolation by distance model (Wright 1943). Isolation by distance is defined as a situation in which biological distance

increases with geographic distance. Isolation by distance will occur when populations are relatively non-mobile and inter-population gene flow is restricted. Using dental metric and nonmetric data, I test whether an isolation by distance model explains Classic Maya population structure.

Hypothesis #2: Classic Maya population structure can be explained by an isolation by distance model.

Considering the regional variation in Classic Maya culture, an isolation by distance model may explain population history in the region. On the surface, all Classic Maya sites share some unifying characteristics—use of hieroglyphic writing, the long count, divine kingship, etc. Yet there are obvious regional discontinuities in Maya cultural patterns. The underlying assumption is that the regional patterns in Maya material culture, coupled with evidence from the epigraphic record, indicate a greater degree of historical interaction within zones than between them (Houston 1993; Matthews and Willey 1991; Schele 1991). By extension, we can expect that the populations within a given archaeological zone to be more similar to one another than those located in distant archaeological zones. This similarity would be expected due to both a shared ancestry of populations within each zone and greater intra-zone gene flow, than inter-zone gene flow, during the Classic period.

For this hypothesis to be valid, Classic period Maya populations must have been relatively non-mobile, with gene flow limited to neighboring Maya sites. If isolation by distance describes Classic Maya population structure, the results of the multivariate dental nonmetric and metric analyses will show that Maya sites within a zone were more closely related to one another

than they were to sites from other archaeological zones. In addition, biological distance between Maya sites will be correlated to geographic distance.

In cases where regional populations are relatively isolated from one another, genetic drift, as opposed to gene flow, will dominate population structure. Thus, zones with high levels of gene flow among the populations of the region will exhibit low levels of population differentiation. In contrast, regions with low levels of gene flow will exhibit greater among-group variation. F_{ST} values are one way of measuring among-group variation and I will use F_{ST} values derived from the dental metric data to test Hypothesis #2.

If Hypothesis #2 is rejected, it will demonstrate that isolation by distance does not appropriately describe population structure in the Maya region. In this case, significant gene flow must have occurred across the ancient Maya area, both within and between archaeological zones. Such events might have involved major population movements across zones, either as part of a single major emigration event or as continuous moderate to low level gene flow throughout Preclassic and Classic times.

There is substantial archaeological and hieroglyphic evidence to suggest that Hypothesis #2 will be rejected. When the demographic profiles of Classic period sites are considered, it is clear that they are not uniform—some sites exhibit variable periods of population growth and decline (Culbert and Rice 1990). These fluctuations in population size may reflect episodes of emigration into and out of Classic Maya sites, due to the differences in the fortunes and misfortunes of ancient Maya polities (Demarest 1992, 1997; Fash and Stuart 1991; Houston 1993; Jones 1991; Lucero 1999; Martin and Grube 1995, 2000; Schele 1991; Stuart 1993).

The hieroglyphic record is an important source of information regarding gene flow across Maya zones. Episodes of elite visitation to faraway sites were commonplace (Culbert 1991; Martin and Grube 2000; Schele and Mathews 1991). Oftentimes, these visits re-affirm

political alliances through participation in religious events. For instance, Panel 19 of Dos Pilas (Pasión Zone) describes an event in which the ruler of Calakmul (Central Zone) was present at Dos Pilas to oversee a bloodletting ritual (Houston 1993: 115). However, these royal visitations did not necessarily involve the exchange of genes.

Better evidence for gene flow is described in the inscriptions regarding foreign marriages, typically involving the exchange of daughters from one royal dynasty to another. A clear case of long distance bride exchange occurred at Copan (Southeastern Zone). There, inscriptions indicate the mother of Yax Pasaj Chan Yoatt, one of Copan's final kings, was from faraway Palenque (Northwestern Zone)—effectively, she moved from one end of the Maya world to the other (Fash and Stuart 1991: 167; Martin and Grube 2000: 209). This is just one example of long distance marriage documented in the Classic Maya hieroglyphic record.

Warfare events also deserve mention. One of the goals of Maya warfare was the taking of captives (Webster 2000: 106). The majority of captives, who were presumably sacrificed, were male. However, evidence from two known sculptural depictions of female captives and a female captive figurine from Jaina suggest that females may also have been captured during war (Miller and Martin 2004: 178). Although they might also have been sacrificed, captive females may have served as mates, either at the site of conquest or at the home site of the invaders. Although most war-related inscriptions pertain to conflicts between neighboring sites, some far-flung battles are mentioned, such as the twin defeats that Palenque (Northwestern Zone) suffered at the hands of Calakmul (Central Zone) (Martin and Grube 2000: 159-61).

More recently, oxygen and strontium stable isotope evidence has provided new insight on Classic period migration in the Maya area. Although only the sites of Kaminaljuyu, Tikal, Altun Ha, and Copan have been tested to date, an interesting pattern is emerging that suggests

that migration was greatest during the Early Classic period and included both elites and non-elites (Buikstra, et al. 2004; Valdés and Wright 2004; White, et al. 2001; Wright 2004a).

Thus, when the archaeological, hieroglyphic, and stable isotope data are taken in conjunction, there is substantial evidence for gene flow across the Maya area, both within and between archaeological zones. Therefore, if Hypothesis #2 is rejected, I will examine the results of my multivariate biological analyses of dental nonmetric and metric variation in light of the current archaeological, hieroglyphic, and isotopic data to provide new insight on Classic Maya population history.

POPULATION HISTORY

If (1) dental metric and nonmetric data exhibit significant variability between Maya sites and (2) that biological variability does not follow a simple isolation by distance model, then the biological data will be used to explore population history in the Maya area. As reviewed in Chapter II, our present understanding of Maya archaeology points toward a complex history of interaction for sites within and between archaeological zones. By linking the biological data to the archaeological and hieroglyphic data, we will be in a better position to understand Preclassic and Classic period processes that shaped ancient Maya civilization. Below, I raise just some of the questions that persist in the study of Maya population history. Since each of these issues was touched upon in the review in Chapter II, I do not reiterate that information in the discussion here, rather I focus on how the biological data might be used to answer these questions.

Central Zone

- *As the major Classic period superpowers, did the large sites of Tikal and Calakmul experience high levels of gene flow with other parts of the Maya world?*

Both Tikal and Calakmul grew rapidly during the Early Classic period to become the dominant powers in the Maya world by the Late Classic period (Culbert, et al. 1990; Folan, et al. 1995; Martin and Grube 1995). This growth may be due to (1) the natural population growth of these sites with no gene flow from outside, (2) gene flow from smaller centers and rural areas situated near each respective center, or (3) large scale emigration from across the Maya area. If the third scenario is correct, Tikal and Calakmul will have relatively small biological distances with many other Maya sites and will plot near the centroid of any biological distance map. If affinities are demonstrated between Tikal and/or Calakmul and other Maya sites, it will be interesting to determine whether these associations correlate to known alliances during the Classic period (Martin and Grube 2000). For instance, Tikal and Copan were allies, Piedras Negras was part of the Calakmul hegemony, and Dos Pilas was first founded by Tikal and later subjugated by Calakmul. At present time, it is unclear exactly what the function of these alliances was. Did they simply enhance the social prestige of the overlords, or did they come with broader economic and political benefits? The biological data may help clarify some of these issues by illustrating whether the hegemonies of Tikal and Calakmul resulted in greater than expected gene flow between each of the respective superpowers and their subordinates.

Usumacinta Zone

- *Can the population explosion at Piedras Negras be explained by immigration from the Central Zone?*

Houston and colleagues (2003) raised the possibility that the late Early Classic population explosion at Piedras Negras was the result of a major population influx from the Central Petén. However, Golden et al. (2004) have more recently suggested that the Classic period population

booms at Piedras Negras and other primate centers in the Usumacinta Zone was due to immigration from local secondary sites. If Houston et al. are correct; Piedras Negras will demonstrate low biological distance with the sites of the Central Zone. However, if Golden et al.'s model is valid, Piedras Negras will not plot with the Central Zone and will be relatively isolated from other sites in the study sample.

Pasión Zone

- *Was the Late Classic Dos Pilas population comprised of immigrants from the site of Tikal?*

Hieroglyphic inscriptions from Dos Pilas identify the founder of the dynasty as a member of Tikal's royal family, yet the settlement data from Dos Pilas suggests that the population of Dos Pilas was comprised of local people (Houston 1993). If the population from Dos Pilas originated in the area, they will demonstrate biological affinities with other Pasión sites. However, if the founder of the Dos Pilas was accompanied by a substantial group of emigrants from Tikal, the population of Dos Pilas will demonstrate a small biological distance from Tikal.

- *Was the Terminal Classic renaissance at Seibal and Altar de Sacrificios due to an influx of individuals from outside the Pasión Region?*

Changes in artifact and iconographic styles at Terminal Classic Seibal and Altar de Sacrificios led members of the Harvard University projects at these sites to conclude that after A.D. 800 the site was invaded by foreigners from the Gulf Coast (Sabloff 1973; Sabloff and Willey 1967; Tourtellot 1990a; Willey 1990). If a foreign invasion did occur at Seibal and Altar de Sacrificios, we would expect the Terminal Classic component of these sites to demonstrate large biological distances with other sites from the Pasión Zone, and possibly one another. Further, the influx of foreign immigrants will increase the overall biological variability of the

Pasión, resulting in increased F_{ST} values. Recent hypotheses suggest the Terminal Classic renaissance at Seibal was due to a take over of the site by individuals from the Maya site of Ucanal (Schele and Matthews 1998; Tourtellot and González 2004). Without comparative samples from Ucanal, it is difficult to predict how this would affect population variability at Seibal.

Belize Zone

- *Does the cultural variability of Belize correspond to biological differences between sites of this zone?*

Some Belizean sites demonstrate evidence for heavy cultural and material exchange with the Central Zone during the Classic period, whereas others appear removed from this zone. Of the sites included in this study, Colha demonstrates the greatest degree of interaction with sites from the Petén—Late to Terminal Classic Colha ceramics are similar to Central Zone ceramics (Valdez 1987) and Colha lithics were traded into the Central Zone (Hester and Shafer 1994). If this interaction involved the settlement of people from the Central Zone at Colha, we would expect Colha to cluster with Central Zone sites in the biological plots. Otherwise, Colha should demonstrate its greatest affinity to the other Belizean sites. However, I must take caution in all of my interpretations of the Colha sample since there is a possibility that it is represented by non-local people (see Chapter V).

Southeast Zone

- *Can the Classic period population boom at Copan be explained by immigration from either Tikal or Kaminaljuyu?*

Researchers have suggested that the Classic period fluorescence may have been fueled by a major immigration of people from the Tikal area (Longyear 1952). Recent excavations in the epicenter of Copan have uncovered tombs with artifacts demonstrating a strong affinity to the Central Petén, particularly Tikal (Bell, et al. 2004; Reents-Budet, et al. 2004; Sharer 2004; Sharer, et al. 1999). Valdés and Wright (2004) have raised the possibility that people abandoning Preclassic Kaminaljuyu migrated to Copan, joining populations that were already there. Fash and Stuart (1991) contend the Classic period occupation at Copan was a local development. If the Classic period population explosion at Copan was due to a population infusion from the Tikal area, we would expect Copan to exhibit a small biological distance from that site. If Copan received a large number of immigrants from the highlands at the end of the Late Preclassic period, it should demonstrate a biological affinity with the highland site of Kaminaljuyu. However, if the Classic period population of Copan was comprised largely of descendants of local populations, it should appear relatively distinct from other Maya samples.

Highlands

- *Was the cultural exchange between the highland site of Kaminaljuyu and Tikal and Copan accompanied by gene flow between the two areas?*

Elite burials at Kaminaljuyu share features in common with lowland Maya sites, particularly Tikal and Copan, and include individuals that have isotopically been identified as foreigners (Valdés and Wright 2004). If the cultural exchange with Tikal and Copan involved a large scale movement of people, we would expect Kaminaljuyu to demonstrate biological affinity with the lowland sites it interacted with. However, if this cultural exchange merely involved the trade of goods and ideas, with only a few instances of immigration, Kaminaljuyu should appear relatively distinct in the multivariate biological analyses.

Pacific Coast

- *Was the Pacific Coast comprised of populations with strong biological affiliations with the lowland and highland Maya?*

The material culture of the Pacific Coast indicates the area was engaged in extensive interaction with other parts of Mesoamerica (Bove 1989a). As a result, it has been difficult to identify the ethnic identity of its inhabitants. Preclassic antecedents of Classic period Maya culture can be found on the Pacific Coast. However, the Classic period Pacific Coast lacked many of the cultural markers characteristic of Classic Maya society and is generally not thought of as "Maya." If the Pacific Coast populations sampled here were biologically related to populations in the Maya lowlands, we should expect them to exhibit relatively small biological distances with other Maya samples. However, if the Pacific Coast was inhabited by non-Maya people, or by a Maya people ancestrally distinct from populations in the lowlands, the Pacific Coast should demonstrate large biological distances from other samples in this study.

SUMMARY

In this chapter I provided an overview of the research questions and biological models that are the focus of this dissertation. I use ancient Maya skeletal samples as proxies for ancient populations in order to reconstruct population history in the Maya area. Although some fundamental differences exist between skeletal populations and true biological populations, I argue that these differences are adequately controlled for in this research and reasonable reconstructions of population structure and history can be achieved. Building upon our current knowledge of Maya population history, I develop a series of three key research hypotheses that I explore in this dissertation. The first hypothesis establishes the validity of using dental nonmetric and metric data to analyze ancient Maya population structure and history. The second

hypothesis determines whether ancient Maya population biological variability follows a simple isolation by distance model. If the second hypothesis is not supported, I will use the results of the multivariate analyses to provide new insight on Maya population history from a biological perspective. In the last part of this chapter, I outlined some of the current questions in Maya population history and illustrated how these issues can be addressed with biological data.

CHAPTER IV

BIOARCHAEOLOGICAL APRROACHES TO ANCIENT HUMAN POPULATION VARIABILITY

This chapter provides a brief summary of previous research on human population variation, focusing on dental metric and nonmetric analyses. This chapter is divided into four sections. The first discusses what is presently known about the inheritance of dental size and morphology. The second reviews previous dental anthropological studies of human population variation, emphasizing work in the New World. The third section discusses the history of ancient population variation studies in Mesoamerica. The final section addresses recent theoretical developments in studies of ancient population variation pertaining to the integration of methods and theory borrowed from population genetics.

The study of human skeletal morphometric variability, also known as biological distance or biodistance, is as old as the field of physical anthropology itself. Early morphometric studies of the skeleton were pre-occupied with creating racial typologies for organizing human populations from around the world. According to Buikstra and colleagues, "skeletal biodistance studies examine variation in bone or tooth shape and form in order to define patterns that are thought to reflect genetic relatedness within or between past populations" (Buikstra, et al. 1990: 1). More recently, biological distance researchers have adopted terminology from population genetics to characterize their studies. Thus, biological distance becomes divided into population history and population structure. Population history pertains to the genetic or phenotypic history of a population or populations as a whole. Population structure relates to the organization of the populations themselves. That is, are the populations united by gene flow or are they separated from one another and subjected to drift? Clearly, the study of population history is not exclusive

of population structure, and vice versa. In this dissertation, I refer to population history and population structure, as well as the more traditional terminology of biological distance.

In this project, I use phenotypic characters of the skeleton to study ancient population history. Ideally, it would have been useful to use two entirely different and functionally unrelated aspects of the skeleton with minimal correlation of character; for instance craniometrics and dental morphology. However, due to the poor nature of skeletal preservation in the Maya region, it is extremely difficult to obtain sufficiently large sample sizes for conducting biological distance analyses based on bony, as opposed to dental, characteristics of the skeleton. In addition, the ancient Maya practice of artificially deforming the cranium severely inhibits the use of the skull in biological distance studies. In contrast, teeth are generally well preserved in the Maya area. Further, due to the ancient Maya's heavy reliance on processed maize foodstuffs, Maya skeletons demonstrate only slight to moderately worn teeth (Scherer, et al. 2004). Thus, dental measurements and morphological observations can be readily made on middle aged and old adults. Due to these circumstances, I have opted to use dental morphology and measurements in my analysis of ancient Maya population history. Since dental nonmetric and metric traits are used in this study, the following discussion of human biological variation focuses on these phenotypes.

With few exceptions (Lukacs and Hemphill 1991; Powell 1995; Rhoads 2002; Wrobel 2003), most dental studies of ancient biological variability focus on either dental measurements or dental morphology, but rarely both. Incorporating more than one biological dataset increases the robusticity of the results. Each phenotypic data set comes with its own set of strengths and weaknesses. For instance, dental nonmetric traits have been shown to be highly heritable, generally do not vary between the sexes, yet they are difficult to observe with even moderate attrition and do not readily lend themselves to model-bound approaches to the study of

population history. In contrast, dental metric traits can be observed in worn teeth (particularly bucco-lingual measurements) and are easily incorporated in model-bound approaches, yet are highly susceptible to problems resulting from missing data.

GENETIC CONTROL OF DENTAL MORPHOLOGY AND SIZE

Since teeth are highly heritable, have functional significance, and are better preserved than other aspects of the skeleton, they are used extensively for the purposes of phylogenetic studies in biology, paleontology, anthropology, and related fields. As a result, extensive research has been conducted over the past century in order to understand the genetic mechanisms underlying the development and inheritance of tooth size and morphology. One of the key issues for researchers interested in mammalian dental morphology is the evolution of heterodonty. Mammalian dentition is characterized by its differentiation into three different classes: incisors, canines, and molars (which, in most taxonomic contexts, include premolars). For different species, the number of teeth in each class and their respective morphology vary depending on the dietary adaptation of the organism in question (Hillson 1986). In order to explain this phenomenon, two competing theories were developed: the field concept model and the clone model.

In the field concept model, Butler (1939; 1957) hypothesized that in the earliest stages of development all teeth have the potential to develop into any of the classes of teeth. However, as tooth germs distribute themselves around the maxilla and mandible, some substance or morphogen, specific to different locations within the alveolus, would stimulate the germs to develop into the proper tooth class for that particular location. Within each tooth class, genetic information would encode each respective member of the class to develop differently. In contrast to Butler's field model, is Osborn's (1973; 1978) clone model. Based on experimental

ontogenic data from mice, Osborne theorized the existence of three types of primordium. Each primordia gives rise to a different tooth class: deciduous and permanent incisors, deciduous and permanent canines, and the deciduous and permanent molars and premolars. What distinguishes the clone model from the field model is that the three types of primordium are not equipotent, that is they cannot give rise to any tooth class—the identity of the tooth is intrinsic to the tooth germ and is not dependent on some foreign stimuli. According to the clone model, there was a single primordium for each tooth class which was then cloned, giving rise to the other primordia in that tooth class. Although the clone model is strongly bolstered by the present body of experimental evidence, it is likely that both models have some value for understanding tooth development (Scott and Turner 1997; Weiss 1990).

Building upon Butler's field model, Dahlberg (1945) proposed four human tooth classes: incisors, canines, premolars, and molars. Butler had previously combined premolars and molars into a single field. In Dahlberg's model of human dentition, each class has a "key" or "polar" tooth that is more stable, in terms of size and morphology, than the other members of the class. For each tooth class, the most mesial tooth is the polar tooth (e.g. UM1), with the exception of the lower incisors for which LI2 is the polar tooth. In terms of environmental influence, polar teeth are more stable than non-polar teeth. As such, the polar teeth are often the focus of dental metric and morphological analyses (Stojanowski 2001; Turner, et al. 1991).

Recent advances in microbiology have identified a group of genes, known as homeobox genes that appear to control the development of segmented structures (Duboule 1994). Sharpe, Thomas, and colleagues (Sharpe 1995; Sharpe; Thomas and Sharpe 1998; Thomas, et al. 1998) proposed an "odontogenic homeobox gene code" in which different spatial combinations of homeobox genes direct tooth germs to develop into the respective tooth classes. The parallel between Sharpe's model and Butler's field model is apparent. Nonetheless, this model has not

been definitively proven and work on the relationship between homeobox genes and dental patterning is ongoing (Zhao, et al. 2000).

Understanding the exact mode of inheritance for dental traits has proven difficult. It is firmly established that most morphological traits are not under a simple mode of inheritance (i.e. they are not controlled by a single gene loci), despite numerous attempts to identify a dental trait that follows a model of simple inheritance (Kolakowski, et al. 1980; Kraus 1951; Portin and Alvesalo 1974; Turner 1967, 1969). Rather, the fact that dental nonmetrics are quasicontinuous phenotypic traits suggests that it is unlikely that any are controlled by a single gene (Scott and Turner 1997: 136). For instance, the Carabelli's cusp is not simply present or absent, or even absent, small, or large, rather it varies from a small furrow on the lingual aspect of maxillary molars to a complete supernumerary cusp with a freestanding tip.

Thus, a general consensus has been reached that nonmetric traits follow a complex mode of inheritance. Nonetheless, complex segregation analysis has shown that dental morphology is controlled by a relatively limited number of genes, in comparison to more genetically complex phenotypes such as stature (Kolakowski, et al. 1980; Nichol 1989; Scott and Turner 1997). Further, it has been suggested that coding for some traits may be dominated by a single major gene (Scott and Turner 1997). However, in terms of inter-species patterns in cusp morphology, Zhao and colleagues (2000: 165) raise the possibility that specific cusps are unlikely to be controlled by specific genes, but by a dynamic interaction between various genes and signaling factors during ontogeny. Thus, although it appears that a relatively small number of genes are involved in the expression of nonmetric traits, it is unclear how these genes control the expression of these phenotypes.

As a result of the pioneering work of Fisher (1918; 1922), researchers recognized early on that, like the vast majority of continuous phenotypic traits, tooth size is under a polygenic

mode of inheritance (Kieser 1990). Recent research has confirmed this observation. For instance, Kolakowski and Bailit (1981) attempted to identify genetic loci for dental dimensions through segregation analysis of data from a Melanesian population. However, locating gene loci has proven difficult. As a result, the bulk of the research concerning the heritability of dental measurements has focused on assessing heritability values (h^2), as opposed to the exact mode of inheritance (the quantity and location of genes involved).

Familial studies, particularly twin studies, provide an important line of evidence for the strong genetic control of tooth size and morphology (Kieser 1990; Scott and Turner 1997). These studies are typically used in conjunction with a theoretical framework borrowed from the field of quantitative genetics. Specifically, researchers are interested in teasing out the degree to which variability in the characteristics of the teeth are controlled by variation in heredity as opposed to the environment. In twin studies, concordance analysis is often used to compare monozygotic (identical) twins to dizygotic (fraternal) twins (Kaul, et al. 1985; Scott and Potter 1984; Skrinjaric, et al. 1985; Townsend, et al. 1988; Townsend, et al. 1992). Monozygotic twins share both a genotype and an environment, whereas dizygotic twins share an environment but are only fraternally related. Family studies have focused on parent-offspring relationships (Scott and Turner 1997). In these twin and family studies, the heritability of dental traits and size has been found to range from 0.40 to 0.80 (Jordan and Abrams 1992; Scott 1991; Scott and Turner 1997).

Although under strong genetic control, dental size and morphology are also subject to environmental influences. The clearest evidence of this can be observed in occasions of morphological asymmetry, where a given dental trait may exhibit a greater expression on one tooth antimere than on the other. This is especially evident in studies of monozygotic twins where a trait may be more fully expressed on a given tooth for one twin and less so on the same

tooth of the other (Scott and Potter 1984). However, no systematic study exists that characterizes the level of plasticity of dental morphological traits under different environmental contexts. In a study of Norse immigration to the North Atlantic (Iceland and Greenland), Scott and Alexander (1992) demonstrated that differences developed in the craniofacial complex of migrant populations, while dental morphology remained very similar to the parent population. This study suggests that dental morphology is more resistant to environmental influences than more plastic aspects of the skeleton.

The evidence for an environmental effect on tooth size is stronger. There is an allometric association between dental size and body size, which is clearly a reflection of an environmental influence for this dental phenotype. Research on prenatal growth has demonstrated a correlation between size at birth and dental size, such that babies who were born underweight also show diminished tooth size, an observation that holds even for crowns that developed postnatally (Garn, et al. 1979). As noted above, heritability estimates of tooth size range from 0.40 to 0.80, thus evidence for an environmental effect on tooth size is not surprising. What is notable is that studies of ancient skeletal populations document that populations that underwent environmental stress also experienced, in some instances, diminished tooth size (Guagliardo 1982; Simpson, et al. 1990). In these studies, individuals who died as children had smaller tooth dimensions than those who died as adults. As a result, it is critical to test for age trends in the dental metric data if subadult individuals are to be included in a study sample.

A logical question relating to the variation of human dental morphology and size is whether or not evolutionary forces—aside from factors of gene flow and drift—can cause the phenotypic differences observed between populations? Some researchers have suggested that regional differences in dental morphology are in part due to natural selection while others counter that most if not all nonmetric traits offer no selective advantage (Scott and Turner 1997).

For instance, the dental traits that characterize Sinodont (Northeast Asian and American Indian) dentition (shoveling, protostylid, etc.) produce a larger and more complex occlusal surface. This increase in tooth surface may have conveyed an adaptive advantage in the processing of some food types, particularly in hunter-gatherer diets (Guthrie 1996). However, such arguments are merely a priori postulates and do not rely on statistical testing of phenotypic differences under a model of selection. Rather, the current body of evidence indicates that the differences seen in the dental morphology of modern humans is largely a result of random processes (i.e. genetic drift) and that, despite efforts, no trait has ever been clearly demonstrated to incur a selective advantage (Scott and Turner 1997: 254).

Relative to dental morphology, tooth size may be under stronger natural selective pressure. Throughout hominid history, there has been a general decrease in tooth size with time, both between species as well as within *Homo sapiens* (Brace, et al. 1991). Of particular note is the recent size reduction in the past 10,000 years that may be associated with advances in food processing and the transition to agriculture. Three theories have been advanced to explain this dental reduction: the probable mutation effect (PME), the selective compromise effect (SCE), and the increasing population density effect (IPDE) (Brace 1964; Calcagno 1989; Frayer 1978). According to Brace (1964; 1982), the PME posits that there was a selective pressure for the maintenance of large tooth size throughout much of hominid history. However, the development of cooking and later pottery softened much of the food humans consumed, resulting in a relaxation of the selective pressure for large teeth. This follows the argument that larger teeth withstand greater levels of dental wear and remain functional. Central to the PME argument, is the postulate that complex morphological traits, such as tooth size, will diminish as random deleterious mutations accumulate in the absence of natural selective pressure favoring the complex phenotypes. In other words, according to the PME, there was not necessarily a positive

selection for decreased tooth size throughout hominid evolution; rather there was a relaxation of natural selection favoring large tooth size.

In contrast, the selective compromise effect (SCE) posits that natural selection shifted from favoring large teeth to favoring smaller teeth over the course of human history (Calcagno 1989; Calcagno and Gibson 1991). The SCE argues that caries replaced wear as the dominant dental pathology as food became increasingly processed, especially with the advent of agriculture. Thus, the diminished surface area of smaller teeth is thought to reduce the possibility of carious infection. Further, Corruccini (1991) argues that with an increase in food processing comes a decrease in selective pressure favoring large maxilla and mandible that had been needed to support large masticatory muscles used to chew unprocessed food. Thus, smaller teeth are advantageous for smaller jaws as they reduce the opportunity for malocclusion and impaction, which can lead to infection.

In the increasing population density effect (IPDE) model, the reduction in tooth size is associated with worsening health conditions as a result of increased environmental stress (Macchiarelli and Bondioli 1986). As such, reduction in tooth size should occur simultaneously with other skeletal indicators of malnutrition and increased illness, such as stature size reduction. Macchiarelli argues that the reduction in tooth size and stature is genetically based: selection favored individuals of smaller body size.

Of the three models, the IPDE has the least explanatory power in that (1) a diachronic reduction in tooth size and stature is not universally observed across space and through time and (2) there is no evidence to support natural selection for smaller individuals in stressed populations. Rather a reduction in body size is a *physiological* product of the stress (Armelagos, et al. 1989; Gibson and Calcagno 1989). The first two models, PME and SCE, are generally supported in that they correlate with dietary changes and technological innovations in human

history (Brace, et al. 1991; McGee 1984). The critical difference is whether relaxed selection alone can account for the dental size changes (PME) or if active selection is required to change tooth size in the time period proposed by the SCE (Calcagno and Gibson 1988). At the present time, the issue is still unresolved, though it is likely that both models partially explain the reduction in human tooth size during human history.

DENTAL ANTHROPOLOGY AND HUMAN POPULATION VARIATION

There is a long history of research using dental morphology and dental size as a means of studying biological relationships among modern humans and our fossil ancestors. This research grew out of a broader biological interest in using dental variability as a means of characterizing taxonomic differences between organisms, particularly with an eye towards reconstructing evolutionary lineages and identifying modes of adaptation.

The earliest studies of human dental morphology occurred during the nineteenth century, when dental anatomists identified various modern human dental traits, such as von Carabelli's work on the lingual accessory cusp of the upper molars (von Carabelli 1842). Scott and Turner (1997) recognize Hrdlička's (1920) early research on incisor shoveling as the foundation work in anthropology on the variation of human crown morphology. Of particular note was Hrdlička's observation that American Indians and Asians shared a common expression of incisor shoveling, which was generally not observed among Europeans or Africans. From this evidence, Hrdlička was among the first to postulate a common ancestry for modern Asians and American Indians.

Studies of human dental morphology received a major boost when Dahlberg (1956) and Hanihara (1961) established the first systematic procedures and comparative casts for the study of dental traits. Differences in crown morphology were emphasized in the systems of Dahlberg and Hanihara, though variability in root form was also considered. Advancing this

standardization work, Turner, Scott, and colleagues at the Arizona State University (ASU) Department of Anthropology developed the current dental morphological standards and comparative dental casts that are used in essentially all recent and ongoing studies of dental morphology (Turner, et al. 1991).

Studies of human dental morphological variation have been initiated in almost every area of the world occupied by humans, past or present. All inhabited continents have been studied, with examples from North America (Dahlberg 1963; Haydenblit 1996; Jacobi 1997; Powell 1995; Sciulli, et al. 1984; Turner 1993); South America (Brewer-Carias, et al. 1976; Kieser and Preston 1981; Sutter 1997); Asia (Hanihara 1991, 1992; Lukacs and Hemphill 1991); Africa (Greene 1982; Haeussler, et al. 1989; Irish 1997); Europe (Brabant 1971; Goose and Roberts 1982) and Australia (Richards and Telfer 1979; Smith 1981). In addition to these regional studies, dental morphology has also been assessed at multi-regional and global levels, such as Turner's work on the morphological variability of dentition around the Pacific Rim (Turner 1985a; C. G. Turner, II 1990).

In all of these studies, the dental morphology of a series of skeletal samples was compared using multivariate statistics in order to determine patterns of biological distance. The most commonly used statistic for dental nonmetric data is C.A.B. Smith's Mean Measure of Divergence (MMD) (Scott and Turner 1997). Assuming that the distance statistic reveals underlying patterns of biological affinity, the MMD produces a series of pairwise values for each population compared in a study; low values represent a close biological affinity and large pairwise values indicate a large biological distance.

As with dental morphology, there is a long history of interest in the study of differences in modern human dental size. Unlike dental morphology, however, much of the research on dental size has focused on evolutionary changes in the human lineage. Starting with our

Miocene hominoid forbearers and continuing through the Plio-Pleistocene hominids, there is a general reduction in tooth size overtime that has been attributed to a combination of either selection favoring smaller teeth in more modern forms, or a relaxation of selection pressures that were present in the past, as discussed in the previous section (Brace, et al. 1991; Calcagno and Gibson 1991).

Although not as extensively used as dental morphology, dental size has been employed to address issues of biological affinity and population structure in ancient and modern human populations. Research has shown that there are continental differences in tooth size at the global level (Schnutenhaus and Rösing 1998), with Aboriginal Australians exhibiting the greatest tooth size on average, and Europeans and Asians the smallest (Hillson 1996: 82). Dental metric analysis has been used most extensively to examine population differences at the regional level, including Archaic North America (Powell 1995), Ohio (Sciulli 1979), Central Mexico (Christensen 1998c), Belize (Wrobel 2003), India (Hemphill, et al. 1991; Lukacs and Hemphill 1991). However, it has also been used to examine intra-site variation in ancient Honduras (Rhoads 2002), colonial Florida (Stojanowski 2001), and Belize (Jacobi 1996). Typically, researchers prefer cranial metric studies over dental metric studies in quantitative approaches to biological distance. This is largely due to a combination of the wide variety of measurements that can be taken from the skull (Moore-Jansen, et al. 1994), the demonstrated heritability of cranial-facial characteristics (Sjøvold 1984, 1995), their wide applicability in modern forensic contexts (Ubelaker 1998), and the long history of such research in physical anthropology (Howells 1973, 1989; Lahr 1996). Thus, dental metrics are only favored in parts of the world where poor skeletal preservation and/or cranial deformation has affected the measurability of crania. A second factor that complicates studies of dental metrics is the inter-correlation of crown diameters between teeth (Harris and Rathbun 1991). Fortunately, statistical methods

which account for inter-variable correlation, such as principal components analysis or Mahalanobis Distance, can be used to accommodate for this drawback of dental metrics.

Intra-Site, Regional, and Continental Studies of Dental Variation

Both dental metrics and nonmetrics have demonstrated utility in reconstructing population structure and history at the site, regional, and continental levels. For the purpose of brevity, I will summarize work on these different levels of analysis within the Americas with the purpose of providing a general sense of the diversity of applications for the study of ancient dental variation. A discussion of previous research on biological variation in Mesoamerica has been reserved for its own section that follows.

Biological distance studies have addressed intra-site questions of phenotypic variability since the early 1970s (Lane and Sublett 1972; Spence 1974a). These early studies focused almost exclusively on metric and nonmetric variability of the cranium, owing largely to a lack of standardization in dental research at this time. One early exception was Corruccini's (1972) analysis of biological relationships in historic Pueblo populations. Corrucini incorporated a few dental metric and nonmetric variables in a larger battery of skeletal metric and nonmetric traits. In recent years, however, intra-site analyses of dental variability have become more popular, with research focusing on questions of population structure (e.g., kin-structure/class endogamy, post-marital residence patterns, the identification of "foreigners", etc.).

Howell and Kintigh (1996) used variability in dental traits within the Zuni settlement of Hawikku to examine kinship structure at the site. They used both an analysis of nonrandom patterning of the binomial distribution of dental traits in the sample and cluster analysis of individuals to determine whether there was a correlation between patterns of dental traits and cemetery groupings within the site. The identification of a non-random distribution of non-

metric traits was taken as evidence of a kin-structured social hierarchy at Hawikku. However, Corruccini (1998) has criticized their approach on the grounds that they employed a one-tailed binomial probability to test their null hypothesis (when a two-tailed approach would have been more appropriate) and they did not compensate for inter-trait correlation in their univariate analyses.

Taking a more refined statistical approach to kinship analysis using Euclidian distance coefficients, Corrucini and Shimada (2002) used dental nonmetric and metric data to examine phenotypic variability in the Huaca Loro pyramid mound in northern coastal Peru. They studied a remarkably small sample of 29 individuals from a series of nine groups within the pyramid. Oftentimes, intra-cemetery analyses which exploit small samples sizes use univariate approaches to examine differences within and between groups, as in the Howell and Kintigh (1996) study. However, such approaches are prone to Type I errors. Corrucini and Shimada illustrate that a multivariate approach will produce more satisfying results. Corrucini and Shimada's analysis was able to demonstrate non-random patterning of dental metric and nonmetric variability between the nine burial groups. Thus, they argue that class endogamy was practiced by the individuals interred within the pyramid. Unfortunately, it is unlikely that their approach will find wide use in studies of ancient biological variability as it requires each individual to be observable for nearly all of the characters used in the study.

Using dental metric data, Stojanowski (2003b) examined intra-cemetery variability at three colonial sites from the Georgia coast. A novel aspect of Stojanowski's approach is that by using a matrix decomposition model he was able to assess intra-group variability without having to make apriori assumptions about group membership. This is an important distinction in that it permits analysis of intra-site biological variation where no clear archaeological evidence of population heterogeneity is apparent (spatial patterning of the burials, mortuary indicators of

class/ethnic distinction, etc.). Through this approach, Stojanowski was able to estimate the number of sub-populations within the skeletal sample he was studying and argue that both population aggregation and genetic admixture with non-resident groups together produced the observed biological pattern for the mission population he studied.

At the regional level, the majority of research on dental variability has been directed towards answering questions of population history. In the United States, a substantial amount of dental research has been conducted on modern Southwest Indian populations by Scott and colleagues (Scott and Dahlberg 1982; Scott, et al. 1983; Scott, et al. 1988). In general, they have found a correlation between patterns of affinity based on crown morphology and other anthropometric data. Overall these relationships mirrored what was expected based on shared linguistic and cultural systems. However, through a Mean Measure of Divergence (MMD) analysis of dental nonmetric traits, Nichol (1990) demonstrated that, for some samples, gene flow between geographically proximal but culturally dissimilar groups has occurred in the region.

In Ohio, Sciulli and colleagues have conducted substantial research on dental size and morphology of the ancient inhabitants of the region (Sciulli 1979, 1998; Sciulli and Mahaney 1991; Sciulli, et al. 1984). Sciulli and colleagues found substantial homogeneity in dental morphological patterning within ancient Ohio. In comparison to other parts of North America, Ohio is somewhat distinct; indicating a degree of genetic continuity and isolation in the Ohio region (Sciulli, et al. 1984). However, Sciulli (1979) found only moderate correlation between patterns of dental morphology and dental size between populations, which he interpreted to be due to selective processes affecting tooth size during Ohio's prehistory based on further analysis of dental size (Sciulli and Mahaney 1991).

Sutter (1997) examined dental nonmetric variability in prehispanic Andean populations dating from the Archaic period through European contact using a MMD analysis. Sutter identified major chronological differences in dental patterning in some of the regions he examined, that coincide with periods of major socio-political change. This led him to argue that episodes of major political upheaval triggered large-scale migration in some areas, while other regions appear to have been genetically stable.

Recently, Stojanowski (2001; 2003a; 2004) conducted an extensive dental metric analysis of historic period mission populations in Georgia and Florida using Harpending and Ward's (1982) **R** matrix model as modified by Relethford and Blangero (1990) for anthropometric data (see the section below on model-bound approaches for a detailed discussion of the **R** matrix model). He found that in both Florida and in Georgia, initial missionization of local Indian populations resulted in increased phenotypic variability as a result of population aggregation and extralocal gene flow. However, in later mission years, genetic drift reduced genetic variation as a result of a demographic collapse. Stojanowski also compared the mission populations to earlier pre-contact samples to identify the source of the mission populations. What distinguishes Stojanowski's approach from earlier regional studies is that he paid greater attention to both population structure and population history.

At the continental level, dental research in the Americas has been geared towards understanding the origins and affinities of American Indians. The majority of this research has been conducted by Turner and colleagues using dental morphological variability of both modern and ancient American Indians and comparing the American samples to data from Asia (Greenberg, et al. 1986; Scott and Turner 1997; Turner 1985a, b, 1986; C. G. Turner, II 1990; Turner and Machado 1983). Based on these analyses, Turner has identified two relatively distinct "mongoloid" dental complexes: Sundadonty and Sinodonty (C. G. Turner, II 1990).

Eight dental traits are used to distinguish between Sundadonts and Sinodonts: shoveling, double shoveling (UI1); tooth reduction/absence (UM3); deflecting wrinkle (LM1); cusp number (LM2); enamel extension (UM1); and root number (LP3, LM1). Generally, Sundadonts, which include populations from island and mainland Southeast Asia, Australia, the continental shelf of East Asia, and Japan, are characterized by reduced versions or absence of these traits. In contrast, Sinodonts, which include populations from Northeastern Asia and indigenous America, are characterized by more complex expressions of these crown traits and more commonly have single roots for the root traits in question.

Within the American Indian populations studied, Turner detected frequency differences in some dental traits, such as the frequency of three-rooted lower first molars (Turner 1971, 1986). This led him to propose a tri-partite model for the peopling of the Americas. In this model, the first wave of migrants coincided with the Paleoindian period and gave rise to the majority of modern American Indian populations. A second and third wave gave rise to modern Na-Dene and Aleut/Eskimo speakers, respectively. Turner bolstered his argument with linguistic evidence (Greenberg 1987), arguing that this same tri-partite division is seen in linguistic differences of modern American Indians (Greenberg, et al. 1986).

Turner's model is not without its critics. In a discriminant function analysis of dental variability in the New World using Turner's original data, Powell (1995) found that middle Holocene American Indian samples cluster with Sundadonts. Further analysis using biological distance statistics confirmed this finding; middle Holocene American Indian samples do not readily cluster with modern American Indian samples. This contradicts Turner's original model, which suggests that all American Indian samples, regardless of time period, should exhibit the Sinodont pattern. However, Powell (1995: 230) cautions that this does not necessarily indicate an alternative ancestry for earlier American Indian populations, rather it highlights the

morphological distinction of early American Indians and suggests that the evolutionary processes giving rise to modern American Indian biological diversity are more complex than those originally proposed by Turner.

Further evidence for the dental morphological differences between ancient and modern American Indian populations comes from Central and South America. In an analysis of Central Mexican dental variability with samples spanning from 1300 B.C. to A.D. 750, Haydenblit (1996) found that 73% of the traits she studied were more similar to frequencies expected of Sundadont populations. Further, three out of four of the samples in Haydenblit's study were allocated with the Sundadonts by discriminant function analysis. The one sample that was identified as Sinodont, from Cholula, was also the most recent (A.D. 550-750). In Andean South America, Sutter (1997) found that Archaic and Formative period samples tended to be intermediate between Sundadonts and Sinodonts, whereas later period samples were more characteristically Sinodont. These results confirm Powell's observation that earlier populations in the America's are not clearly Sinodont, and only after the equalizing processes of migration and gene flow took affect in the later Holocene did Sinodonty become the characteristic dental pattern for most of the Americas.

PREVIOUS STUDIES OF ANCIENT MESOAMERICAN POPULATION VARIATION

A number of previous studies have been conducted on ancient Mesoamerican population variation. In almost all instances, these studies relied on either dental morphology or dental metrics. The notable exceptions are Spence's analysis of cranial nonmetric variation at the Central Mexican site of Teotihuacan (Spence 1974b, 1994) and Christensen's research on cranial nonmetric variation in Mexico (Christensen 1997, 1998d). The lack of cranial metric and nonmetric studies in Mesoamerica, which are quite popular elsewhere in the world, is a

reflection of two factors. First, preservation in Mesoamerica, particular in the humid tropical Maya lowlands, is generally quite poor and complete crania from excavations are not common. Second, throughout ancient Mesoamerica cranial deformation was practiced, introducing a major environmental (non-genetic) cranial morphological factor that is impossible to control for with present statistical procedures. Fortunately, teeth are generally well preserved in Mesoamerica and tend to exhibit minimal dental wear as a result of heavy reliance on maize agriculture. Although dental modification was commonly practiced in Mesoamerica, it is limited to the anterior teeth and even when modification has occurred; traits of the cingulum (tuburculum dentale, interruption grooves, etc.) tend to be unaffected. For the sake of thoroughness, I include all types of Mesoamerican biological distance studies, including those that relied on cranial nonmetric data.

Among the earliest studies of biological variation in Mesoamerica was Spence's (1974b) analysis of population structure at Teotihuacan using cranial nonmetric traits. Spence examined postmarital residence patterns between apartment compounds at the site. In Spence's model, the mobile sex (i.e., females in a patrilocal system) should exhibit less between-group variation and more within-group variation than the non-mobile sex. In other words, greater between-group distances for males would indicate a patrilocal system. Using the Jaccard formula, Spence found that in almost all cases, males exhibited a greater between-group distance indicating patrilocality for ancient Teotihuacan, which he suggests was based in part on the hereditary nature of craft production at the site.

More recently, Spence (1994) revisited the issue of population structure at Teotihuacan by re-evaluating the cranial nonmetric data using revised sex information. In the La Ventilla B compound, he found that males demonstrated greater homogeneity relative to females, confirming earlier results. This trend appears to have held for other apartment compounds,

though small sample sizes compromise the reliability of these results. Using the Jaccard Square Cumulative Similarity statistic and the Simple Matching Square Cumulative Similarity statistic, Spence also demonstrated a significant degree of heterogeneity between apartment compounds. He interpreted this heterogeneity as evidence of the mosaic nature of the Teotihuacan population; a product of ongoing immigration from outside the city.

Austin (1970; 1978) was the first researcher to examine biological variability between sites in the Maya area. Austin analyzed dental nonmetric traits at the Pasión sites of Seibal and Altar de Sacrificios. The primary goal of his research was to determine whether or not a population intrusion occurred at these sites at the end of the Late Classic period as postulated by Adams (1964) and Sabloff and Willey (1967). Although his sample sizes were limited, Austin (1978) observed greater discontinuity in dental nonmetric traits from the earlier to later periods at Seibal than at Altar de Sacrificios. He attributed the difference to foreign immigration at Seibal but not at Altar de Sacrificios.

Mexican anthropologist Pompa y Padilla (1984; 1990) compared the dental morphology of Chichén Itzá and Jaina—two Maya sites in the Yucatan—to one another as well as to the Guatemalan site of Altar de Sacrificios (using Austin's published data) as well as other non-Maya sites. Interestingly, Pompa y Padilla found little affiliation between the Chichén Itzá and Jaina series, with Jaina exhibiting dental morphology more like that of Altar de Sacrificios far to the south. In terms of methodology, Pompa y Padilla makes a notable diversion from most other studies of dental nonmetric traits. He argues that both the right and left antimeres should be included in the calculation of trait frequencies (Pompa y Podilla 1990: 37-8). However, it is never made clear how he handles instances in which an individual is not observable for both antimeres of a given trait. If this factor of differential preservation is not accounted for, some individuals will be unequally represented relative to others, thus skewing the resulting statistics.

Jacobi (1996; 1997; 2000) analyzed intra-site variation of tooth size and morphology at the colonial Maya site of Tipu, Belize. He found little differentiation in both dental metrics and nonmetrics between individuals buried within the early colonial church and those buried outside its walls, indicating biological homogeneity at the site. Jacobi concluded that all of the interments at Tipu were Maya and that there was no evidence that Spaniards were buried at the site. For the Tipu Maya, Jacobi characterized the common dental non-metric traits of the site, which included: shoveling (UI1), double shoveling (UI1), distal accessory ridge (UC, LC), Carabelli's trait (UM1), hypocone (UM1-UM3), anterior fovea (UM1), Y-X-X groove pattern (LM1, LM2, LM3), and the deflecting wrinkle (LM1). Using a standardized MMD, Jacobi compared the Tipu nonmetric dataset to all of the published Maya dental nonmetric data, including trait frequencies at Seibal (Austin 1978), Altar de Sacrificios (Austin 1978), Lubaantun (Saul 1975), Lamanai (Lang 1990), and a modern sample of Tzeltal Maya (del Ángel E., et al. 1993). He found that four of the series exhibited significant differences from Tipu, indicating substantial variability in Postclassic period and early Historic Maya dental morphology.

Haydenblit (1996) examined dental morphology in four populations from Central Mexico (Tlatilco, Cuicuilco, Monte Albán, and Cholula), looking for differences among these populations. She also included Turner's (1983; 1986; 1987) data on dental morphology from around the Pacific Rim in her study. Based on MMD analysis, Haydenblit demonstrated that Tlatilco, the oldest sample in the study, was the most divergent from the other samples. Haydenblit suggests the divergence of Tlatilco represents either (1) a partially different parent population(s) for the site relative to the other sites or (2) the temporal distance between Tlatilco and the other sites in the study.

Christensen analyzed dental metric and cranial nonmetric variation in Mexico to answer questions pertaining to the population history of the Valley of Oaxaca (Christensen 1998a, b, c)

and the Basin of Mexico (Christensen 1997). In his analysis of Oaxacan biological variation, Christensen used a battery of univariate and multivariate statistical analyses. For his cranial nonmetric study Christensen used MMD and principal components analysis. In the dental metric component of his study, Christensen used Haldane's equation, coefficients of variation, Lande's equations for selective mortality and effective population size under a model of genetic drift, and principal components analysis. Christensen found a cranial non-metric similarity between the coastal Río Verde Valley and the highland Early and Middle Formative Oaxacan Valley samples (Christensen 1998b). He interprets these results to support predictions of Formative period population dispersal based on linguistic evidence. However, Christensen also detected substantially smaller tooth sizes among inhabitants of the Río Verde Valley than their highland contemporaries which he attributes to natural selection favoring smaller tooth size, a process he also observed working throughout the settlement history of the Oaxacan Valley (Christensen 1998c).

Recently, Rhoads (2002) analyzed dental metric and nonmetric variability at the Classic Maya site of Copan. Using Bayesian discriminant analysis, Rhoads was unable to provide correct barrio classifications based on dental metric or nonmetric data. In other words, dental patterning was not notably different between barrios at Copan. This result is not surprising since population structure would need to be substantially prominent to be detected with dental metric and nonmetric data (Scott and Turner 1997). Rhoads calculated biological distance between barrios using Mahalanobis D^2. She then compared the resulting biological distance matrix to a geographic distance matrix for the barrios and found a very low statistical correlation, indicating that geographic distance is not a good predictor of biological distance at Copan. Here again, it is difficult to say whether this is attributable to a true lack of isolation by distance, the low strength of dental data for identifying population structure, or a combination of the two. However,

principal components analysis of the metric data did detect intra-site heterogeneity. Along the first component, individuals clustered into one of two distinct groups. When the site membership of these individuals was considered, Rhoads found that in the majority of cases (18/26), entire sites fit into one of the two clusters with no overlap, contra to the findings of her Bayesian analyses. Rhoads (2002) interprets this to represent the presence of two lineages within the Copan pocket.

Rhoads compared her Copan nonmetric data to published Maya data from Tipu (Jacobi 2000) and the Yucatán (Turner 1985a), as well as other Central American sites (Turner 1985a) using Nei's distance and MMD analysis. Rhoads found that Copan best clustered with Tipu, which is to be expected based on cultural similarities (they are both Maya) and geographic proximity. However, the remaining sites clustered together, all of which were scored by Turner. Thus, it is possible that inter-observer error, which was not tested, might have affected the results. Further, Rhoads found few statistically significant differences between the samples using MMD analysis. This demonstrates the importance of using a region-specific nonmetric trait dichotomization scheme, as opposed to the standard dichotomization scheme used by Turner (1986), to better highlight any differences in dental morphology within a relatively circumscribed region.

The first truly regional study of dental variation within the Maya lowlands was conducted by Wrobel (2003) who analyzed dental variation in northern Belize. Wrobel analyzed population history in northern Belize using dental metric and nonmetric data that he collected from the sites of Chau Hiix, Altun Ha, and Lamanai. Prior to any analysis of biological distance, Wrobel documented a temporal reduction in tooth size, particularly the posterior teeth, from the Preclassic through Historic periods. Wrobel attributes this trend to selective pressure favoring smaller teeth, noting that a reduction trend is "commonly found among agricultural populations

over a long period of time" (Wrobel 2003: 76). However, judging by Wrobel's linear plots of dental size change, very little of this reduction occurs within the Classic period (Wrobel 2003: Figures 6.1-6.4). When he analyzed the linear trend by pooling the sites for each time period and comparing the groups with Penrose size and shape coefficients, he did not find a meaningful pattern in the data. In other words, the smallest distances were not found between consecutive periods (i.e. Preclassic to Early Classic). Although Wrobel attributes the lack of a meaningful pattern to small sample size, intra-site differences in dental size and/or a significant lack of a chronological trend in dental size reduction may also account for the observed results. In fact, when the site of Lamanai alone is considered, the Penrose shape coefficient does produce the expected results. This suggests that although a chronological trend may be present in northern Belize, intra-site differences in dental size outweigh an overall trend in size reduction, contra Wrobel's (2003) conclusion.

When Wrobel pooled his odontometric data for northern Belize by time period and compared the results to Altar de Sacrificios and Early and Late samples from the site of Seibal in Guatemala and the historic site of Tipu using Penrose size and shape coefficients, he achieved conflicting results depending on the combination of traits used. Wrobel attributes this to a lack of strength for odontometrics in Maya regional analyses. However, the problem may lie in the nature of the archaeological groups compared (specifically the pooling of all northern Belize samples). Moving beyond the Maya area, Wrobel compared his Maya samples to data from Central Mexico and South America. In this analysis, Seibal and Altar de Sacrificios consistently clustered together and away from the northern Belize sample, indicating regional odontometric differentiation in the Maya area. However, the northern Belize sample often clusters with Central Mexican groups as opposed to other Maya groups, which call into question whether the odontometric data is actually reconstructing real population history.

Wrobel (2003) analyzed biological distance based on dental nonmetric data by combining all of the northern Belize samples, separated by time period, and compared these samples to published data on other Maya sites and to data he collected for Seibal. Although Wrobel used a standardized MMD, he does not use the Green and Suchey (1976) angular transformation to control for differing sample sizes, a practice that has become standard in dental nonmetric studies (e.g., Haydenblit 1996; Irish 1993; Nichol 1990; Prowse and Lovell 1996; Rhoads 2002; Sutter 1997). Rather, he follows an older procedure used by Buikstra (1976) and Jacobi (2000). Nonetheless, his results do show regional trends in morphological diversity, with the Belizean samples clustering together, and with historic Tipu and Seibal the outliers. In an analysis of Terminal Classic populations alone, Wrobel found a small distance between the Guatemalan sites Altar de Sacrificios and Seibal, as well as a small distance between the northern Belizean sites of Chau Hiix and Lamanai, again confirming a regional trend in morphological diversity. Oddly, Altun Ha, another northern Belize site, was an outlier. When Wrobel compared the Maya data to published data from Central Mexico (Haydenblit 1996; Pompa y Podilla 1990), South America (Sutter 2000), and Turner's (1985b) large database of North and South American Indians, the Maya sites consistently clustered together. These results demonstrate the diversity of dental morphology in Mesoamerica and the affinity of Maya sites to one another, indicating shared ancestry and/or extensive gene flow within the Maya area.

More recently, Cucina and Tiesler (2004) conducted an odontometric analysis of Maya biological affinity that incorporated data from both the southern and northern Maya lowlands. They collected data from the Classic period sites of Xcambo in northern Yucatan, Calakmul in northern Petén, and a pooled Southeast Petén sample; as well as colonial samples from colonial Campeche and Tipu (from Jacobi's [2000] published data). In addition, they included a comparative control sample from the pre-ceramic site of Cueva Roja, Dominican Republic.

Cucina and Tiesler used a combination of cluster analysis, multidimensional scaling, and neighbor-joining methods in their study. Although the details of the clusters vary with each type of analysis, some general patterns emerged from their study. First, Calakmul and the Southeastern Petén samples consistently grouped together. Second, the colonial samples of Campeche and Tipu repeatedly clustered with one another. Third, the Cueva Roja control sample always plotted as an outlier, as expected. The main difference in all of the plots was the position of the northern Yucatan site of Xcambo, which variably clusters with either the colonial samples (Campeche and Tipu) or plots as an outlier. Cucina and Tiesler suggest this may reflect the unique position of Xcambo as a trade node with connections throughout eastern Mesoamerica. Overall, Cucina and Tiesler's (2004) study highlights odontometric differences in the Maya area that relate to either geographic or chronological differences. However, without additional samples it is impossible to say which process is more strongly contributing to the differences observed.

As a final note on ancient Mesoamerican studies of biological diversity, I observe that despite the great interest in ancient DNA studies in the Maya region—few analyses have been conducted in the region and these studies have met with limited results. Two factors inhibit ancient DNA research in the Maya region. First, hot and humid environments, such as the Maya lowlands, are notorious for their poor preservation of ancient DNA (Kumar, et al. 2000). Second, curation of Maya skeletal materials, especially in Guatemala, is often less than ideal and many of the remains have undergone extensive post-excavation handling and consolidation, which further degrades the integrity of the DNA and contaminates it with modern DNA. Even under ideal circumstances, researchers at Copan were able to recover DNA in less than 50% of their attempts (Merriwether, et al. 1997). Thus, until significant strides are made in ancient DNA analyses such that DNA can be reliably and readily extracted from ancient Maya skeletons,

the focus of research on population structure and history in the Maya area will, by necessity, rely on phenotypic characters of the teeth and skeleton.

MODEL-BOUND VERSUS MODEL-FREE APPROACHES

Traditionally, studies of ancient biological distance by physical anthropologists have taken a "model-free" approach, to use terminology that was first coined by Relethford and Lees (1982) and has become commonplace in recent literature (Powell and Neves 1999; Stojanowski 2001). In model-free analyses, interpretations of biological affinity are based solely on inferences of phenotypic similarity between two samples. In other words, statistics are derived to determine which samples are most phenotypically alike and then historical interpretations are derived from these results. Typically, model-free approaches posit gene flow as the primary determinant for phenotypic similarity. Thus, samples that are phenotypically similar are inferred to have a recent common ancestry and/or to have experienced ongoing gene flow between the samples, whereas samples that are phenotypically dissimilar are so due to a lack of common ancestry and/or gene flow. For instance, in Turner's (1985a; 1985b; 1986; 1990) analysis of the origins of American Indians, similarities between modern American Indians and populations in northeastern Asia are taken as evidence of common ancestry for *all* American Indians at *all* time periods. However, Turner's position has been criticized on the grounds that little consideration was made for the possible effect of population structure on early populations in the New World and the role of genetic drift on shaping American Indian biological diversity (Powell 1995). By nature of the statistics, model-free approaches are typically concerned with issues of population history and do not address population structure (but see Lane and Sublett 1972; Spence 1974a).

Although model-free approaches make intuitive sense, they do not account for all of the factors that can affect the phenotypes of ancient populations. Most notably, model-free

approaches fail to consider the effects of genetic drift, a function of population size. When populations are small, allele frequencies can rapidly fluctuate from one generation to the next, whereas in large populations, allele frequencies are more constant and may often become "fixed" (Hartl and Clark 1997). Thus, the allele frequencies of small populations are also more subject to additional evolutionary forces, such as gene flow and selection. In model-bound approaches, the goal is to realistically model the evolutionary and demographic parameters using population genetics theory. Thus, in addition to producing distance statistics, model-bound approaches identify population genetics parameters such as *F*-statistics and migration rates. As a result, model-bound approaches can more appropriately address issues of population structure (Conner 1990; Konigsberg 1988; Konigsberg and Buikstra 1995; Powell and Neves 1999).

The most widely applied model-bound approach stems from Harpending and Ward's (1982) **R** matrix model. The **R** matrix model, as originally devised for allelic data, is based on the analysis of observed and expected population heterozygosity for a geographic region. Expected heterozygosity for each population is derived from the total heterozygosity of the geographic region. Thus, a comparison of expected versus observed heterozygosity can be used to assess levels of gene flow, where greater observed than expected levels of heterozygosity indicate greater than average gene flow. This model was revised for quantitative phenotypic traits by Relethford and Blangero (1990) and has since been applied in a wide variety of studies using phenotypic data from skeletons (Powell and Neves 1999; Relethford and Harpending 1994; Steadman 1998; Stojanowski 2004).

One of the fundamental parameters of model-bound approaches is the estimation of effective population size. For the **R** matrix model, the results are scaled by effective population size in order to remove the possible effects of drift in small populations. Effective population size is a theoretical population size that is used for population genetics modeling (Hartl and

Clark 1997). The effective population size is the ideal population size that behaves the same as the real population size. However, the effective population size is almost invariably smaller than the real population since in real populations some individuals have different fitness levels, some individuals do not mate, inbreeding reduces the randomness of allelic distribution, etc. In living populations, effective population size is calculated from demographic parameters of the real population. However, in skeletal studies little is often known about the demographic structure or actual size of ancient populations. Further, the skeletal samples used in model-bound approaches are multi-generational and are thus not true breeding populations. In the **R** matrix approach discussed above, each sample is weighted by an estimated population size. In some cases, reasonable historical data are available on population size and can be used (Stojanowski 2004). More often, the relative population sizes are derived from archaeological estimates (Powell and Neves 1999; Relethford and Harpending 1995; Steadman 1998).

Heritability of phenotypic traits is another variable that must be factored into model-bound approaches to ancient biological variability. As the heritability of traits can vary by population, it is impossible to determine actual heritability rates for phenotypic traits, such as dental traits, for the specific populations studied. For dental traits, current data indicate a heritability range of 0.40 to 0.80 for the stable teeth within each tooth class (Scott and Turner 1997: 164). Similarly, estimated heritability for tooth size ranges as high as 0.60 to 0.80 (Scott 1991). Although some studies run multiple statistical analyses and vary the level heritability in each run, Relethford and Blangero (1990) found that when using the **R** matrix statistic the model was little affected by differing heritability estimates.

Should model-bound approaches be used to the exclusion of model-free approaches? From a strictly theoretical perspective, assuming the derived mathematical models are correct, they should produce more accurate reconstructions of ancient biological history than model-free

approaches. However, although the inclusion of additional genetic and demographic parameters in model-bound approaches should lead to improved results, it also involves the incorporation of an increasing number of unknown variables. Unfortunately, no study has actually been conducted that evaluates the model-bound and model-free approaches used by physical anthropologists on a population with known demographic and evolutionary parameters, thus the relative empirical value of each approach remains untested.

I would argue that the perspective taken by Powell and Neves (1999) represents the approach that most physical anthropologists should take in their research on ancient population variability. In their study of the peopling of the New World, both model-free and model-bound approaches are employed to determine whether the different approaches will produce alternative conclusions. According to Powell and Neves (1999: 178), "we use the model-bound approach simply as a *heuristic device*, with attention to how the samples may or may not meet stated assumptions, and how alteration of model parameters affect the pattern of genetic relationships observed" (emphasis in the original). In their conclusions, they weigh the assumptions and results of both approaches in formulating their argument for the origins of American Indians. When effective population sizes in the model-bound approach were considered equal, very similar results were achieved between the model-bound and model-free analyses (Powell and Neves 1999). However, when effective population sizes were altered in the model-bound statistics to reflect a smaller population size for Paleoindians, alternative results were obtained. Although this study did not definitively prove the superiority of model-bound approaches, they showed the critical importance of considering population size in studies of biological diversity. Nonetheless, it remains advisable to incorporate both approaches to strengthen the validity of any results.

SUMMARY

Extensive analyses of the heritability of teeth have demonstrated a strong genetic component for both tooth size and morphology. Heritability estimates of both dental size and morphology have been found to range between 0.40 and 0.80 (Scott and Turner 1997). As a result, both dental metrics and nonmetrics have enjoyed a long history of use in reconstructions of ancient population structure and history.

Population studies of dental metric and nonmetric variation have occurred at the intra-site, regional, and continental level, answering questions pertaining to both population structure and population history. In this dissertation, I am interested in issues of population history as it pertains to the origins and trajectory of site populations within the Maya area, as well as population structure in regards to differing levels of gene flow and isolation across the region.

Previous studies of biological diversity in Mesoamerica have documented statistically significant variability in the region. In particular, recent studies of dental morphology in the Maya region have demonstrated substantial phenotypic differences even within this relatively restricted area. Nonetheless, these earlier studies struggled with a number of methodological problems, including the use of sites with small sample sizes and the selection of an inadequate number of sites to answer the proposed research questions. Further, significant portions of the Maya area remain untested. This study seeks to remedy this problem by incorporating data from across the Maya area and includes the largest sample size to date for the region.

One area of caution noted in Wrobel's (2003) study is the possible presence of a chronological trend in dental size reduction in northern Belize, from the Preclassic to the Historic period. A similar trend was noted for Central Mexico by Christensen (1998c) in the Valley of Oaxaca. As a result, it will be necessary to test for chronological trends in the dataset employed here before proceeding with any biological distance analysis using dental metric data.

CHAPTER V

ANCIENT MAYA SKELETAL SAMPLES

This study incorporates 977 dentitions from 18 sites located across the Maya region. I made an effort to select as many available sites as possible for each of the archaeological zones to be tested in this analysis. However, I placed an emphasis on sites with large, well documented skeletal samples. Although it would have been ideal to have an equal number of sites and skeletons from each archaeological zone, I was confined by differences in sampling across the Maya area.

In this chapter, I provide an overview of the skeletal samples used in this study. For each site, I provide a brief description of the site, a review of the history of archaeological research at each of the site, information about how demographic data was obtained, the source of the site's mortuary context information, and details about how population estimates were made by investigators at each site. Additional archaeological information about the sites discussed here is available in Chapter II.

For the majority of the sites, I used sex and age determinations made by other researchers. However, in a few instances it was necessary for me to make demographic determinations. I followed standard procedures for the osteological estimation of age and sex (Buikstra and Ubelaker 1994). Since Maya skeletal remains are almost invariably poorly preserved, it is often not possible to estimate sex or age. Positive sex identifications were reserved for cases where multiple diagnostic elements of the pelvis and/or cranium were available for observation. In no instance did I use discriminant functions of long bone measurements to estimate sex. The determination of age for subadults was straightforward; relying almost exclusively on dental development. For adults, diagnostic elements of the pelvis

were often not available and cranial suture closure can be affected by deformation. Thus, in many cases I simply noted that an individual was adult and when possible determined their relative age—young (18-35 years), middle (36-50 years), or old adult (>50 years)—from the level of skeletal and dental degeneration.

When possible, I relied on age and sex data collected by other researchers. Of particular importance was Wright's bioarchaeological study of the Pasión Zone (Wright 1994). Demographic data for all of the Pasión burials was extracted from her dissertation (Wright 1994, 2004). However, in a few cases Wright determined sex using a dental discriminant function. Clearly, it will not be possible to accurately test for sexual dimorphism in tooth size when tooth dimensions are used to determine sex. Therefore, I only used the sex determinations that were made from pelvic and carnial morphology, rather than incorporate any of the determinations that were based on the dental discriminant function. In addition to the Pasión sites, I used age and sex data collected by other researchers for Calakmul, Altun Ha, Colha, and Kaminaljuyu. More about the demographic data of these sites is given in the discussion that follows.

The age and sex distribution of the skeletal sample is presented in Table 5.1. For the majority of the skeletons, sex cannot be determined. For many of the sites there is a bias towards males in the sample. This is likely due to a bias in the sample, with many of the skeletons coming from the monumental core of the sites. As would be expected, the majority of the skeletons in the sample are from adult individuals.

In addition to demographic information, data were collected on mortuary context and chronology. These data were extracted from both published and unpublished sources. Although

Table 5.1. Age and sex distribution of the Maya dental sample.

Site	Archaeological Zone		Male	Female	Indet.	Total	Location
Tikal	Central	Subadult: Adult:	--- 10	--- 12	54 222	**298**	• Museo Nacional, Guatemala • Tikal National Park, Guatemala • University Museum, U of Pennsylvania
Uaxactun	Central	Subadult: Adult:	--- 2	--- 2	2 5	**11**	• Museo Nacional, Guatemala • Peabody Museum, Harvard University
Calakmul	Central	Subadult: Adult:	--- 16	--- 4	6 16	**42**	• Universidad Autonoma de Yucatan, Mexico • Universidad de Campeche, Mexico
Piedras Negras	Usumacinta	Subadult: Adult:	--- 11	--- 14	30 38	**93**	• Piedras Negras Laboratory, Guatemala • University Museum, U of Pennsylvania
Dos Pilas	Pasión	Subadult: Adult:	--- 20	--- 9	5 18	**52**	• Salon 3, Instituto de Antropología e Historia Warehouse, Guatemala
Aguateca[1]	Pasión	Subadult: Adult:	--- 5	--- 4	1 7	**17**	• Salon 3, Instituto de Antropología e Historia Warehouse, Guatemala
Tamarindito[2]	Pasión	Subadult: Adult:	--- 4	--- 1	3 3	**11**	• Salon 3, Instituto de Antropología e Historia Warehouse, Guatemala
Itzán	Pasión	Subadult: Adult:	--- 2	--- 3	0 4	**9**	• Salon 3, Instituto de Antropología e Historia Warehouse, Guatemala
Seibal	Pasión	Subadult: Adult:	--- 25	--- 6	5 3	**39**	• Peabody Museum, Harvard University
Altar de Sacrificios	Pasión	Subadult: Adult:	--- 25	--- 10	12 14	**61**	• Peabody Museum, Harvard University

Table 5.1. Continued.

Site	Archaeological Zone		Male	Female	Indet.	Total	Location
Barton Ramie	Belize	Subadult: Adult:	--- 7	--- 4	9 26	**46**	• Peabody Museum, Harvard University
Baking Pot	Belize	Subadult: Adult:	--- 2	--- 1	2 7	**12**	• Peabody Museum, Harvard University
Colha	Belize	Subadult: Adult:	--- 9	--- 8	8 18	**43**	• TARL, University of Texas
Altun Ha	Belize	Subadult: Adult:	--- 21	--- 24	38 49	**132**	• Department of Anthropology, Trent University, Canada
Copan	Southeastern	Subadult: Adult:	--- 3	--- 0	7 42	**52**	• Peabody Museum, Harvard University
Kaminaljuyu	Highlands	Subadult: Adult:	--- 0	--- 2	17 16	**35**	• Peabody Museum, Harvard University • Salon 3, Instituto de Antropología e Historia Warehouse, Guatemala
Balberta	Pacific Coast	Subadult: Adult:	--- 0	--- 1	1 7	**9**	• Salon 3, Instituto de Antropología e Historia Warehouse, Guatemala
Montana Complex[3]	Pacific Coast	Subadult: Adult:	--- 0	--- 2	6 7	**15**	• Salon 3, Instituto de Antropología e Historia Warehouse, Guatemala
TOTAL			**162**	**106**	**709**	**977**	

[1]The Aguateca sample includes 8 skeletons from Qui Chi Hilan and 1 skeleton from Cerro de Cheyo.
[2]The Tamarindito sample includes 4 skeletons from Arroyo de Piedra.
[3]The Montana Complex is comprised of skeletons from the Los Chatos, Manantial, and Paraíso complexes.

I only present detail on chronological data to the level of archaeological period, I also collected ceramic phase information when it was available. However, since each archaeological site has its own ceramic phase sequence and a significant number of burials cannot be dated to that level, I do not use ceramic phases in this study. The chronological distribution of the sample is presented in Table 5.2.

The majority of the sample dates to the Late and Terminal Classic. For the purposes of this analysis, I only use skeletons from the Classic period. This was done to limit the chronological time span in the study in the event there is an evolutionary trend in the dental metric or nonmetric data caused by selection or drift. Thus, 80 Preclassic and 34 Postclassic individuals were excluded from the analysis. However, for the sample from Balberta some Protoclassic (Late Preclassic) individuals were included (see the discussion of the Balberta sample for an explanation).

POPULATION ESTIMATES AND RANKING

In the late 1950s and early 1960s, Mayanists became seriously interested in issues of settlement and demography following survey work at Dzibilchaltun (Andrews 1965), Tikal (Carr and Hazard 1961), and the Belize River Valley (Willey, et al. 1965). This research established that Maya sites were not vacant ceremonial centers; rather they were home to hundreds if not thousands of people. Interest in Classic Maya demography was further sparked by the discoveries of the Tikal Sustaining Area Project which found substantial settlement in the area around Tikal's urban core, leading its members to estimate that greater Tikal was home to as many as 40,000 people (Haviland 1965; Puleston 1973; Puleston 1983).

For the model-bound analyses of population history in this dissertation, I will need population estimates for each site used. Here, I am interested in maximum Late Classic

Table 5.2. Chronological distribution of the dental sample.

	Archaeol. Zone	Late Preclassic	Early Classic	Late Classic	Terminal Classic	Unknown Classic	Postclassic	Unknown	**TOTAL**
Tikal	Central	17	92	144	12	29		4	**298**
Uaxactun	Central	1		2	6			2	**11**
Calakmul	Central	1	2	12	13	14			**42**
P. Negras	Usumacinta	1	18	73		1			**93**
Dos Pilas	Pasión			30	22				**52**
Aguateca	Pasión			17					**17**
Tamarindito	Pasión			11					**11**
Itzán	Pasión			9					**9**
Seibal	Pasión	5		8	26				**39**
Altar	Pasión	15	7	11	28				**61**
B. Ramie	Belize	9	3	25	6			3	**46**
Baking Pot	Belize							12	**12**
Colha	Belize	5			37			1	**43**
Altun Ha	Belize	13	34	40	28	5	10	2	**132**
Copan	SE		5	43		4			**52**
Kaminaljuyu	Highlands	5	23	7					**35**
Balberta	P. Coast		7	1	1				**9**
Montana	P. Coast		1	14					**15**
Total		**72**	**192**	**447**	**179**	**53**	**10**	**24**	**977**

population sizes. Following the early survey work of the 1950s and 1960s, settlement studies and demography has become a central area of investigation in Maya research (Culbert and Rice 1990). Rice and Culbert (1990) provide an overview of the methodologies used in reconstructing Classic Maya population size. I paraphrase this overview here.

The basic formula for estimating the size of a Maya site involves counting the number of structures at the site, determining when those structures were used, estimating what percentage of structures were occupied simultaneously, and using an estimate of the number of people per household. The Classic Maya typically built their houses on raised stone platforms, which are relatively easy to identify and survey. Since the surface architecture at Maya sites represents the last period of occupation, population estimates are easiest for the Late and Terminal Classic periods. In order to derive population estimates for earlier occupations, it is necessary to test excavate a sample of structures to determine what percentage contain earlier occupation.

In their review, Rice and Culbert (1990) identify a number of the problems in estimating population size at ancient Maya sites. First, some structures are missed during survey—either because they are not detectable on the surface or because they were missed by surveyors. Thus, researchers typically add 10% to 50% more structures to their total structure counts before calculating population size. Another problem is that not all structures were residences. Most researchers estimate that 5 to 30% of structures were not occupied and downsize their estimates of household structures accordingly. Another source of disagreement regards the estimate of the percentage of house structures that were simultaneously occupied. Estimates range from 70 to 93% of structures being contemporaneously occupied. Finally, researchers use different figures for the number of individuals per Maya household. The most commonly cited figure is 5.6 individuals/household, which is derived from the ethnographic work of Redfield and Villa Rojas (1934). Currently, most researchers accept an estimate of 4.0 to 5.6 individuals per house.

For the majority of the sites in this study, population estimates are already available. I describe how these estimates are derived for each site in the review that follows. Unfortunately, due to disagreements regarding methodology, not all population estimates are directly comparable. Besides the problems noted by Rice and Culbert (1990), another source of error in comparing ancient Maya population estimates are differences in the extent of the site used in population estimates. At most Maya sites, population estimates focus on the mapped area. However, very large, politically significant Maya sites possess what has been termed a "sustaining area"—a region of surrounding settlement that supported the sociopolitical center (Satterthwaite 1951). The regularly cited population estimates for Tikal (Culbert, et al. 1990), Calakmul (Folan, et al. 1995), and Copan (Webster and Freter 1990) include these sustaining areas, whereas the estimates for most other sites pertain primarily to the site center, defined as the monumental core and immediate surrounding settlement. This is typically the area shown on site maps.

For the statistics that I will use to reconstruct ancient population variability, I do not need *absolute* population size estimates to be accurate. Rather, it is essential that the *relative* population size for each site is correct. It is not important, for the purposes of my statistics, whether Tikal was home to 10,000, 50,000, or 100,000 individuals. Rather it is critical that I know the relative size of the Tikal population in comparison to other sites. Was Tikal two, five, or ten times the size of Piedras Negras? Thus, I have chosen to develop a population ranking system. My population rankings and the original archaeological population estimates are presented in Table 5.3.

Table 5.3. Late Classic-Terminal Classic maximum demographic estimates. Population estimates are from published sources. Population ranks are my own based on structure counts at each site.

	Population Estimate	Number of Structures	Population Rank	Source
Central Zone				
Tikal	13,275 (62,000)[1]	3,382	0.695	(Culbert, et al. 1990: 116)
Calakmul	24,315 (50,000)	4,863	1.000	(Fletcher and Gann 1992: 23; Folan, et al. 1995: 310)
Usumacinta Zone				
Piedras Negras	2,500	386	0.079	(Houston, Escobedo, Child, et al. 2003: 217)
Pasión Zone				
Altar	300	77	0.015	(Smith 1972: 187)
Seibal	7,577	707	0.145	(Tourtellot 1990b: 102)
Dos Pilas	3,000	492	0.101	(Palka 1995: 406)
Belize Zone				
Altun Ha	2,733	516	0.106	(Pendergast 1979: 24)
Barton Ramie	1,400	262	0.054	(Willey, et al. 1965: 570)
Colha	4,000	710	0.146	(Eaton 1982: 13)
Southeastern Zone				
Copan	5,797-9,464 (22,500)	1,071	0.220	(Webster and Freter 1990: 55)
Highlands				
Kaminaljuyu	6,500	1,300	0.267	(Michels 1979a: 296)
Pacific Coast				
Combined Balberta—Montana Complex	NA	200	0.041	(Bove and Medrano 2003: 55)[2]

[1]For Tikal, Calakmul, and Copan the first population estimate represents the site core and surrounding "suburban" settlement. The second estimate represents the greater site area, including rural settlement. The latter estimate is what typically appears in the literature.
[2]See the discussion of the Pacific Coast samples for details on the derivation of the population rank.

For this system, I use a count of the number of structures within the mapped area of each site. A few sites—Tikal, Calakmul, Copan—have known sustaining areas beyond the mapped core. For these sites, I do not included structures beyond the archaeologically recognized core of the site, which is defined for each site in the discussion that follows.

The advantage of using a population rank, as opposed to population archaeological estimates, is that I avoid methodological inconsistencies between studies regarding the percentage of coevally occupied structures and the number of inhabitants per structure. Rather, I need only assume that these two figures were relatively equal for all sites. I include ceremonial monumental architecture in my tabulations, even though many of these structures clearly were not households. I have done so for two reasons (1) at smaller sites it is difficult to distinguish between ceremonial and non-ceremonial architecture and (2) we would expect the number of ceremonial structures to increase with population size. I checked my rank determinations against the original population estimates to determine if comparable results were obtained.

For the purposes of the multivariate statistics, it would be fine to leave my population ranks as raw structure counts. However, in order to better visualize the relative population sizes between each site I have rescaled the structure counts for each site by dividing each site's count by the structure count of the largest site. In this case that site is Calakmul. Thus, the number of structures at each site was divided by 4,863. This value is my final population rank.

A review of Table 5.3 shows that both the population ranks and the original population estimates generally maintain the same relative population differences between the sites. This is not surprising since the population estimates were derived from these structure counts. Nonetheless, by comparing structure counts, as opposed to population estimates, I have eliminated any error that may result from comparing population estimates that were derived from different demographic equations.

CENTRAL ZONE

Tikal

Situated in the heart of the lowlands in central Petén, Tikal is one of the most important sites in the Maya area. By the height of its power during the Late Classic period, it is estimated to have had a population of approximately 62,000 inhabitants (Culbert, et al. 1990). From the Late Preclassic period on, Tikal was a major power in the central Petén. By the Late Classic period, the rulers of Tikal had consolidated a series of alliances that stretched across the Maya lowlands in an ongoing struggle with their arch-nemesis, Calakmul (Martin and Grube 1995, 2000). As in most of the Maya area, however, monumental construction and hieroglyphic inscriptions ceased in the middle of the ninth century and by the end of the century, Tikal was all but abandoned (Harrison 1999).

Tikal is perhaps the most extensively studied of all ancient Maya sites. Aside from early probings in the late 19th and early 20th century, the first major expedition to Tikal was conducted by the University Museum of the University of Pennsylvania from 1955 to 1969. The excavations at Tikal were first directed by Ed Shook (1955 to 1961), followed by a single season under the leadership of Robert Dyson (1962), with William Coe directing the latter years of the project (1961-1969). The University of Pennsylvania focused much of their efforts on the core of the site, including the North Acropolis and Great Plaza (Coe 1990; Shook 1986), the Central Acropolis (Harrison 1970, 2003), and the East Plaza (Jones 1996). However, the University Museum Tikal Project was one of the first Maya archaeological expeditions to seriously investigate households (Becker 1999; Haviland 1985). The University Museum expedition also produced a detailed map of the central area of Tikal (Carr and Hazard 1961) and conducted survey into its periphery, which produced some of the first data on rural settlement in the Maya lowlands (Fry 2003; Puleston 1983). As a result of this settlement research, our understanding

of Maya settlement was revolutionized—what were once thought to be vacant ceremonial centers are now known to bustling urban sites.

From 1979 to 1989, work resumed at Tikal under the direction of Juan Pedro Laporte, with support from the Guatemalan government. This new Tikal project, the Proyecto Nacional Tikal, focused much of its efforts in the Mundo Perdido complex and adjacent areas, as well as some work in the northern part of the site (Laporte and Fialko 1985). Since the 1990s, two small scale projects of excavation have taken place at Tikal, both headed by Guatemalan archaeologists. The first focused on consolidation of Temple I (Muñoz 1998). The second involved consolidation and explorations in Temple V (Gómez 1999).

As a result of four decades of rigorous archaeological investigation, Tikal possesses one of the largest burial series in the Maya area with over 400 burials (Wright, et al. 2003). As a result of the interest in both monumental and domesticate architecture, the mortuary sample is also one of the most diverse. Tikal boasts a considerable time depth, with monumental architecture appearing at the end of the Middle Preclassic period in the Mundo Perdido complex (Laporte and Fialko 1995). As a result, there are a number of Preclassic burials and the Early Classic period is well represented in comparison to other Maya sites where the vast majority of the burials are limited to the Late Classic period.

Presently, the skeletons of the University Museum Project are stored at the Tikal National Park and at the University Museum in Philadelphia. The skeletons from the Proyecto Nacional Tikal and subsequent Guatemalan investigations are housed at the Museo Nacional de Historía e Etnología and the Tikal National Park. Although both projects readily excavated burials when they were encountered, the University Museum Project disposed of a large portion of the skeletal remains they excavated at the site (Wright personal communication, 2004). As a result, the majority of the individuals housed at University Museum are only represented by teeth

with little associated skeletal material. This explains why 90.1% of the adult dental sample comes from unsexed individuals at Tikal (Table 5.1).

Age and sex data for the Tikal skeletal remains were collected by Wright as part of her bioarchaeological study of the site. This data is available in her progress reports (Wright, et al. 2003; Wright, et al. 2000) and unpublished notes. With the aid of research assistants, myself included, Wright compiled a database of burial context information for the Tikal mortuary sample. This database was available to me for this study.

The Tikal dental sample includes a total of 298 skeletons. Of these individuals, 42 come from problematic deposits and caches at the site. Context information for these skeletons is highly variable, depending on whether they have been published in the Tikal reports and if so, at what level of detail. To further complicate things, it is not clear whether all of the individuals in the caches and problematic deposits of Tikal are local inhabitants or if any of the skeletal remains come from other sites, perhaps as trophies or sacrifices (Becker 1992). Thus, I have chosen to separate the caches and problematic deposits and remove them from the multivariate analyses.

Culbert and colleagues (1990) estimate a maximum Late Classic population of 62,000 people for Tikal. This estimate includes both the central 16 km^2 of Tikal's settlement, which corresponds to the Carr and Hazard (1961) map of the site, as well as the surrounding 104 km^2 support area. They used the standard methodology for estimating Maya population size as outlined in the previous section.

In estimating a population rank for Tikal, I use a structure count from only the 16 km^2 area of the Carr and Hazard (1961) map. Clearly, this area does not include all of Tikal proper, but provides the most realistic comparison available for structure counts from other sites. Rather than counting every structure on the massive Tikal map, I use Culbert and colleagues' data on

structure density of the Tikal map (Culbert, et al. 1990: 116). They indicate that the central 9 km^2 area contains 235 structures/ km^2 and the surrounding 7 km^2 area contains 181 structures/ km^2. From these figures, I estimate a total of 3,382 structures for the central portion of Tikal. For the same area, Culbert and colleagues estimate a population of 13,275 individuals.

Uaxactun

Like its neighbor Tikal, Uaxactun was emerging as a major Maya center in the Late Preclassic period. From this time into the Early Classic period, these two sites were peers and rivals. However, by the beginning of the Late Classic period, Tikal eclipsed Uaxactun and the site remained in the shadow of its powerful neighbor. Like Tikal, Uaxactun spiraled into ruin by the middle of the ninth century.

Uaxactun was first excavated by archaeologists from the Carnegie Institution of Washington from 1926 to 1937 (Ricketson and Ricketson 1937; Smith 1950). This expedition conducted some of the earliest scientific excavations in the Maya area, focusing on the center of the site. This work produced some of the earliest, and still important, data pertaining to monumental architecture (Ricketson and Ricketson 1937; A. L. Smith 1937; R. Smith 1937), settlement (Wauchope 1934), and chronology (Smith 1955) in the Maya lowlands. Further excavations were conducted by the Proyecto Nacional Tikal during the 1980s (Valdés 1986).

I collected dental data from the Uaxactun skeletons excavated by the original Carnegie Institution which are currently housed in the Peabody Museum of Harvard. Unfortunately, the Uaxactun skeletons are incomplete and in a poor state of preservation. I made all age and sex determinations. Mortuary context information was extracted from Welsh's (1988) report on ancient Maya burial practices.

I did not obtain population estimates for Uaxactun because the site is not used in any of the biological distance analyses due to its small sample size.

Calakmul

With only Tikal as a peer, Calakmul was one of the largest and most powerful Maya sites during the Classic period. Situated in the northern part of the Petén, Folan and colleagues (1995) estimate that Calakmul was home to approximately 50,000 inhabitants during the height of its power. Like Tikal, Calakmul possessed a wide-reaching network of political alliances that extended to such far away sites as Dos Pilas and Quirigua (Braswell, et al. 2004). However, by the end of the ninth century, Calakmul fell into a rapid decline from which it never recovered—the population dropped dramatically, monumental construction had ceased, and stelae were no longer erected.

Calakmul has only recently received serious archaeological attention. The first Proyecto Calakmul began in 1984 under the direction of William Folan of the Universidad Autónoma de Campeche and lasted until 1994. The Proyecto Calakmul focused its efforts on survey and mapping, as well as the excavation and reconstruction of the monumental core, with limited excavations outside of the core (Folan, et al. 1995). In addition, the Proyecto Calakmul conducted a detailed study of Calakmul's hydrologic system, climate, and ecology (Braswell, et al. 2004; Gunn 1995). Since 1994, the Mexican Instituto Nacional de Antropología e Historía (INAH) has maintained a project at Calakmul under the direction of Ramón Carrasco. The INAH project has focused primarily on the excavation and reconstruction of the monumental core (Carrasco 1998; Carrasco, et al. 1999).

As a result of the focus on the monumental core of the site, the majority of the Calakmul burials come from high status locales dating to the Classic period, though the actual range of

mortuary treatments vary from simple interments to elaborate tombs (Tiesler 1999). The Calakmul skeletal series has been fully studied by Tiesler as part of her doctoral dissertation (Tiesler 1999) and in ongoing bioarchaeological research of the site in collaboration with Cucina (Cucina and Tiesler 2003, 2004). Tiesler kindly provided the age and sex data as well as the mortuary context information used in this analysis.

Based on Fletcher and Gann's (1992) demographic analysis, Folan and colleagues (1995: 310) estimate a population of 50,000 individuals for the 122 km^2 that comprised greater Calakmul. In estimating population at Calakmul, Fletcher and Gann (1992) used the same methodology as that reported for Tikal (Culbert, et al. 1990) to ensure direct comparability. When just the 21.25 km^2 urban and suburban core is considered, Fletcher and Gann estimate 24,315 individuals from the 4,863 structures identified for the central area.

USUMACINTA ZONE

Piedras Negras

Piedras Negras was one of the central powers controlling the middle Usumacinta river region during the Classic period. Hieroglyphic inscriptions point towards Piedras Negras' dominance of the middle Usumacinta area as early as the Early Classic period (Martin and Grube 2000). Piedras Negras reached its apogee during the Late Classic period, particularly the 7th and early part of the 8th centuries. During this time period, population soared, monumental construction occurred at a dizzying rate, and the hieroglyphic inscriptions of the site record a series of military victories against neighboring sites in the region (Houston, Escobedo, Child, et al. 2003). However, the latter half of the 8th century was a time of turmoil at Piedras Negras—rulership became unstable, diet changed dramatically, social competition increased (Scherer, et al. 2004). In A.D. 808, Piedras Negras suffered a military defeat at the hands of its arch-rival,

Yaxchilan, from which it never recovered and the site was abandoned soon thereafter (Houston, Escobedo, Child, et al. 2003; Stuart 1998).

Piedras Negras was first excavated from 1931-1937 and in 1939 by the University Museum of the University of Pennsylvania, first under the direction of J. Alden Mason and later Linton Satterthwaite. The University Museum concentrated their project efforts on excavating the monumental core of the site, documenting and removing many of Piedras Negras' monuments, and mapping the site (Mason 1933; Satterthwaite 1933, 1936, 1938, 1943). Archaeologists returned to Piedras Negras from 1997 to 2000 in a joint Brigham Young University-Universidad del Valle project headed by Stephen Houston and Héctor Escobedo. The Brigham Young-del Valle project was a large scale endeavor that focused excavations in both the monumental core, the immediate surrounding residential neighborhoods, and in the periphery (Escobedo and Houston 1997, 1998, 1999, 2001; Houston, Escobedo, Child, et al. 2000; Houston, et al. 1998; Houston, et al. 1999; Houston, Escobedo, Terry, et al. 2000).

The original University Museum project produced a sample of ten burials. The Brigham Young-del Valle project supplemented this sample with an additional 108 burials. Although the burials excavated by the University Museum are primarily from the monumental core of the site (Coe 1959), the Brigham Young-del Valle burial sample is a diverse mix of simple interments and elaborate graves from a variety of contexts (Houston, Escobedo, Scherer, et al. 2003). As the project osteologist for the Brigham Young-del Valle project, I, along with Lori Wright and Cassady Yoder, conducted a complete osteological analysis of the site. We determined age and sex for all of the Piedras Negras skeletons from that project (Scherer, et al. 2004; Scherer, et al. 1999, 2001). In addition, I collected dental and demographic data for four individuals from the University Museum project, which are currently housed at the museum in Philadelphia. I

compiled the mortuary context data for Piedras Negras from field burial forms and research reports (Coe 1959; Escobedo and Houston 1997, 1998, 1999, 2001).

Houston and colleagues (Houston, Escobedo, Child, et al. 2003: 217) estimate a Late Classic population of approximately 2,000 to 3,000 individuals for the central core of Piedras Negras. This estimate is based on a figure of roughly five individuals per building and a structure count of 386 structures for the central area of Piedras Negras, corresponding to the University of Pennsylvania map of the site. They evaluate their figure by estimating the number of burials that may be located at Piedras Negras, which they determine to be about 5,000 interments. I use the structure count of 386 buildings in my population rank.

PASIÓN ZONE

Altar de Sacrificios

The site of Altar de Sacrificios was strategically located on the southern bank of the Pasión River, about a kilometer upstream from its confluence with the Salinas River. The site is moderate in size, with three main plaza groups and a series of carved monuments. The site was occupied from Preclassic times until at least the beginning of the Terminal Classic period (Willey 1973a). The hieroglyphic record of Altar de Sacrificios spans from A.D. 455 to 771 and describes the reign of at least ten rulers (Matthews and Willey 1991). It appears that Altar de Sacrificios remained independent of the Petexbatun polity (Demarest, et al. 1997). Although the final monument of Altar de Sacrificios dates to A.D. 771, settlement appears to have continued and fine paste ceramics have been recovered, indicating a Terminal Classic occupation (Willey 1973a).

The first major archaeological expedition into the Pasión region was the Peabody Museum's work at Altar de Sacrificios from 1958 to 1963 under the direction of Gordon Willey

(Willey 1973a). The Peabody Museum project focused their efforts on the monumental core of the site, with test excavations in surrounding domestic groups. A map of Altar de Sacrificios had previously been prepared by Harry Pollock, Ledyard Smith and Ed Shook in 1937.

The Peabody Museum skeletal collection from Altar de Sacrificios consists of individuals from 136 burials (Saul 1972; Wright 2004b). Due to the Harvard University Project's emphasis on the central core of the site, 64% of the excavated burials come from ceremonial or public architecture (Wright 1994). Thus, there is likely a sample bias in the Altar de Sacrificios dental sample for high status individuals. The skeletons of Altar de Sacrificios were analyzed by Wright for her doctoral dissertation (Wright 1994). In addition, she compiled all of the mortuary context information for Altar de Sacrificios. This data was made available for my research.

An area of roughly 1.5 km^2, which includes 77 structures, was mapped and investigated at Altar. Although it possible that settlement extends beyond this area, a settlement drop-off is apparent based on the site map and Willey and Smith (1969: 22) indicate that they only know of one other house mound beyond the extent of the map. Smith (Smith 1972: 187) estimates that of the 77 structures, 54 were residences. Using Redfield and Villa Roja's (1934) figure of 5.6 individuals per Maya household, Smith (1972) estimates a Late Classic population size of 300 individuals for Altar de Sacrificios. I use the total structure count of 77 structures in my population rank.

Seibal

Seibal was one of the most powerful and important sites in the Pasión region. Occupation at Seibal began in the Preclassic period and continued through the Terminal Classic period. In A.D. 735, the king of Seibal, Yich'ak Balam was captured by the king of Dos Pilas

and the site was effectively incorporated into the broader Petexbatun kingdom (Houston 1993: 115; Martin and Grube 2000: 61). However, unlike the rest of the Petexbatun which fell into decline at the close of the Late Classic period, Seibal thrived in the Terminal Classic period. During this time, Fine Orange ceramics appeared at Seibal and stylistically the monuments took on a different appearance (Tourtellot and González 2004). Initially observations of these changes led some researchers to speculate that Seibal fell to foreign invaders, possibly Maya from near the Gulf of Mexico (Sabloff 1973). However, many researchers see no evidence of foreign invasion, arguing these changes at Seibal are simply representative of broader transformations that affected all of the Maya area during the Terminal Classic period (Schele and Matthews 1998: 179; Tourtellot and González 2004).

From 1963 to 1968 the Peabody Museum continued their explorations of the Pasión Zone by moving to Seibal were excavations proceeded under the direction of A. Ledyard Smith and Gordon Willey (Willey 1990). Excavations at Seibal focused on the monumental core of the site (Smith 1982) accompanied by intensive test excavations and mapping in the surrounding zone (Tourtellot 1988).

Human remains from 45 burials have been excavated at Seibal. Due to the diverse excavation strategy of the Seibal Project, the site has a mixed sample, with 40% of the burials from the site center and the other 60% came from domestic contexts (Wright 1994). Wright (1994) analyzed the skeletons from Seibal as part of her doctoral dissertation. In addition, she compiled mortuary context information from published sources (Tourtellot 1990a). I use her osteological and mortuary data in this study.

Tourtellot estimates a Terminal Classic population of 7,577 individuals for Seibal (Tourtellot 1990b: 102). Tourtellot's estimate follows the standard methodology presented in Rice and Culbert (1990) and assumes a 90% contemporaneous occupancy. This estimate is

based on a 15.25 km^2 sampled area around the site and includes both central and peripheral settlement from which 707 structures are reported. Thus, this estimate likely includes settlement from a relatively greater area than those obtained for other sites, such as Piedras Negras, that were not as thoroughly surveyed as Seibal. Nonetheless, this estimate preserves the relative population size of Seibal when actual population estimates are considered. I use the count 707 structures in my population rank.

Petexbatun: Dos Pilas, Aguateca, and Tamarindito

The Petexbatun region is an area south of the Pasión River, centered on Lake Petexbatun. The Petexbatun polity is comprised of a series of sites that by the Late Classic period came under the rule of Dos Pilas. Dos Pilas was founded early in the Late Classic period from a splinter group of Tikal's royal family and, for that reason, Dos Pilas shares its emblem glyph with Tikal (Houston 1993: 98). However, Dos Pilas switched its alliance to Calakmul and with that site's help, became the dominant power in the region, subordinating most of the other Petexbatun sites. Tamarindito was one of the sites conquered by Dos Pilas. Tamarindito, along with Arroyo de Piedra, was a major power in the immediate Petexbatun region during the Early Classic and early Late Classic periods (Valdés 1997). However, in A.D. 761 Tamarindito, presumably with assistance from other subjugated sites in the region, defeated Dos Pilas in military conflict. The Dos Pilas dynasty fled to the twin capitol of Aguateca. However, by the end of the Late Classic period the Petexbatun region was embroiled in military conflict and the archaeological evidence from Aguateca indicates that it too came to a violent end. The whole Petexbatun region fell by the start of the ninth century, one of the earliest collapses in the Maya area (Demarest 2004).

Work in the Petexbatun region was conducted under the auspices of the Vanderbilt University Petexbatun Regional Archaeological Project directed by Arthur Demarest and Juan Antonio Valdés from 1989 to 1994 (Demarest 1997). The Vanderbilt project targeted a number of sites including Dos Pilas, Aguateca, Tamarindito, and Arroyo de Piedra. The Vanderbilt project was multidisciplinary, including the excavation of both site cores and surrounding domestic architecture (Demarest 1997; Inomata 1997; Valdés 1997), survey and mapping (O'Mansky and Dunning 2004; Palka 1997) , agricultural and ecological research (Dunning, et al. 1997), bioarchaeology (Wright 1994), and zooarchaeology (Emery 1997).

Skeletal samples are available from Dos Pilas, Aguateca, Tamarindito, Arroyo de Piedras, as well as a few burials encountered during inter-site survey excavations. With an interest towards increasing sample size, I combined the sites of Tamarindito (n=7) and Arroyo de Piedra (n=4) due to their contemporaneity as early centers in the Petexbatun kingdom. Nonetheless, the combined sample size was too small to incorporate this sample in further analyses. In addition, I combined the skeletons from Qui Chi Hilan (n=8) and Cerro de Cheyo (n=1) with the Aguateca sample as these are effectively the same site (Wright 2003, personal communication). However, the Aguateca sample remained too small to include in further statistical analyses.

As part of her dissertation research, Wright (1994) excavated and analyzed the skeletons of the Petexbatun project. She reports that the vast majority of the Dos Pilas burials come from residential structures, indicating that if there is a bias in the burial sample, it is to nonelite individuals. In addition, she compiled mortuary context information from field notes and reports from the Petexbatun project. In this analysis, I use both Wright's osteological data and the mortuary information she compiled.

Palka (Palka 1995: 406) estimates a maximum Late Classic population size of 2,000 to 4,000 individuals for the site of Dos Pilas. Palka's estimate is based on a formula that includes 1 person per 10 meters of living space, 5% added for invisible structures, and 30% subtracted for estimated noncontemporaneous structures. Mapping of the site by Stephen Houston, then of Yale University, identified 492 structures at Dos Pilas (Houston 1993: 36). I use this structure count in my population ranking. Aguateca and Tamarindito are not used in the multivariate analyses, thus I did not obtain population estimates for these sites.

Itzán

Itzán is a relatively small Maya site 6 kilometers to the north of the Pasión River. The site was occupied from Preclassic times through the Terminal Classic period. Evidence from Itzán indicates it remained independent of the militaristic Petexbatun polity (Johnston 2001).

The site of Itzán was excavated in 1988 and 1990 by Kevin Johnston. The work at Itzán was initiated by the discovery of unplatformed domestic structures exposed during modern road construction (Johnston 1994). As a result, a number of burials were recovered from domestic contexts at the site. Wright (1994) analyzed the skeletons of Itzán as part of her dissertation research. This data, as well as mortuary context information, is available in her dissertation and was used here. Due to its small sample size, Itzán was excluded from multivariate analyses and thus no population estimates for the site have been obtained.

BELIZE ZONE

Altun Ha

The site of Altun Ha is situated in northern Belize near the Caribbean coast. The site is of relatively modest size with a total area of approximately 2.3 km^2. Settlement at the site dates

from the Middle Preclassic through the Terminal Classic period, with some Postclassic occupation (Pendergast 1979). The site probably served as the dominant node in the northeastern Belize coastal zone. Altun Ha is perhaps best known for its evidence of a link with the Central Mexican site of Teotihuacan as demonstrated by the F-8/1 tomb which contained numerous Teotihuacan imports and stylistic artifacts (Pendergast 2003). Interestingly, no other Teotihuacan style deposits are known from Altun Ha.

Archaeological investigation at Altun Ha was directed by David Pendergast of the Royal Ontario Museum from 1964 to 1970. Pendergast's initial impetus for working at Altun Ha was to provide one of the first serious explorations of a Belizean site near the Caribbean coast (Pendergast 1979: 1). Over the course of seven years, Pendergast's team conducted highly detailed excavations and mapping in the central core of the site and its surrounding area (Pendergast 1979, 1982, 1990). The burial sample comes from a diversity of zones throughout the site and thus represents a mix of social groups (Christine D White, et al. 2001). The skeletons of Altun Ha have been extensively studied by Hermann Helmuth, who kindly provided all of the age and sex information used here. Mortuary context information is detailed in the extensive Altun Ha excavation reports (Pendergast 1979, 1982, 1990).

Pendergast (1979: 24) estimates a Late Classic population for Altun Ha of 2,733 individuals. This estimate is based on Pendergast's determination that of the total of 516 structures within the 2.66 km^2 mapped area of Altun Ha, 488 were residential. He uses Redfield and Villa Rojas' (1934) figure of 5.6 people per household in his estimate. Keeping with the methodology that all structures, regardless of function, be considered, I use the larger tally of 516 structures for the purposes of estimating population rank. As with sites like Piedras Negras, the mapped area of Altun Ha does not represent the total extent of settlement at the site, rather it represents the area of primary occupation. Beyond the map, settlement at Altun Ha is scattered

(Pendergast 1979: 15). Thus, even though the value of 516 structures does not represent the total number of mounds at Altun Ha, it is our best value to compare to other sites.

Belize River Valley: Barton Ramie and Baking Pot

Barton Ramie and Baking Pot are among a series of relatively small Maya sites situated in the Belize River Valley in western Belize. Both Barton Ramie and Baking Pot are relatively large sites for the Belize valley. Of the two, Baking Pot is larger with a more elaborate ceremonial center. For the Belize Valley, Barton Ramie and Baking Pot are significant sites, although when compared to Maya sites in this study from other regions these two sites are relatively modest, comprised largely of low mounds (Willey, et al. 1965). Settlement at both Barton Ramie and Baking Pot dates back to the Preclassic period, with a population peak during the Late Classic period (Willey, et al. 1965: 292). Barton Ramie and Baking Pot have not produced hieroglyphic texts nor do they possess standing vaulted structures.

Excavations at Barton Ramie and Baking Pot were conducted as part of the Harvard University Peabody Museum's settlement survey project in the Belize Valley (Willey, et al. 1965). Under the direction of Gordon Willey, this project lasted from 1954 to 1956. The majority of the excavation efforts were directed towards Barton Ramie. Excavations at both sites focused on trenching larger mounds near the center of each site. The site of Baking Pot had been earlier excavated in 1924 by Oliver Ricketson of the Carnegie Institution of Washington (Willey, et al. 1965: 303).

Since all of the burials from Barton Ramie come from residential contexts, it is likely that if there is a sampling bias, it is towards lower status individuals. This is confirmed by the relative paucity of grave goods found with the burials of Barton Ramie (Welsh 1988). Nonetheless, as a relatively minor center, it is unlikely that significant social stratification was

present in Classic period Barton Ramie society. I made all age and sex determination for the skeletons of Barton Ramie and Baking Pot at the Peabody Museum. Unfortunately, the skeletons are poorly preserved and fragmented so it was difficult to obtain demographic data for these sites. I gathered burial descriptions for these two sites from Willey's (1965) survey and excavation report. The sample size from Baking Pot was too small to include the site in any multivariate analyses.

Willey and colleagues (Willey, et al. 1965: 576) estimate a maximum Late Classic population for Barton Ramie at 2,000 individuals. This estimate is based on a count of 262 structures within the Barton Ramie site zone and assumes 7.5 individuals per household, a rather large figure in comparison to other studies. I use the count of 262 structures in my population rank. I did not include Baking Pot in the multivariate analyses and thus no population estimate was obtained for the site.

Colha

The site of Colha is located in northern Belize atop an exposure of high quality chert. Archaeological excavations at the site have demonstrated that its primary economic function was lithic production, supplying stone tools to not only northern Belize but other areas of the Maya lowlands from the Late Preclassic through the Terminal Classic periods (Shafer and Hester 1991). The site of Colha has a long occupation, from the Middle Preclassic through the Postclassic periods (Hester and Shafer 1994). The demise of Colha was a violent one. Evidence from a deposit of decapitated and flayed human crania from Operation 2011 (Massey and Steele 1997) combined with cut, broken, and scattered remains from Operation 2012 point towards at least one episode of systematic killing during the Terminal Classic period (Barrett and Scherer 2004). It has been speculated that this event may have been partially motivated by Colha's

unique position as a major producer and distributor of stone tools (Barrett and Scherer 2004). No hieroglyphic texts are known for Colha.

Colha was first reported by Norman Hammond's Corozal project (Hammond 1973). Under the direction of Thomas Hester of the University of Texas and Harry Shafer of Texas A&M University, Colha was systematically excavated from 1979 to 1994 (Hester and Shafer 1994; Hester, et al. 1994; Shafer and Hester 1983). Much of the efforts focused on Colha's extensive lithic workshops, supplemented by survey, mapping and general investigations of Colha's Preclassic, Terminal Classic, and Postclassic occupations (Hester, et al. 1994).

Colha's skeletal sample consists of a series of 30 crania from a single Terminal Classic deposit (Operation 2011) that was analyzed by Massey (Massey 1989; Massey and Steele 1997), a large collection of Preclassic remains that were unavailable for this study, and a few Classic period burials. The bulk of the Colha skeletal sample used in this study comes from the Operation 2011 deposit. For age and sex information, I collected my own demographic information and cross-checked my results with those obtained by Massey (1989) and found no major inconsistencies. For the remaining burials, I determined age and sex from associated skeletal remains. The Operation 2011 deposit dates to the Terminal Classic period and is well described in the literature (Massey 1989; Massey and Steele 1997; Steele, et al. 1980). I obtained the mortuary context information for the remaining burials from the Colha research reports (Hester 1979; Hester, et al. 1982, 1994).

Eaton (1982) estimates a population of 4,000 individuals for Colha though he is not specific as to how that figure is derived. There is no estimate of the number of structures at Colha, however King (2000) compiled the most complete map of Colha as part of her dissertation work. Using the maps in her dissertation, I counted 710 structures at Colha. It's difficult to say exactly how accurate this figure is. On one hand it seems remarkably high

considering how modest the ceremonial architecture is at Colha. Yet, King (2000) indicates that the map in her dissertation does not include all of the settlement at Colha—some of which is beyond the mapped area and others of which were destroyed in modern times.

SOUTHEAST ZONE

Copan

Copan, located in northwestern Honduras, is one of the largest and most significant Maya sites. Copan is home to some of the finest sculpture and one of the most detailed epigraphic histories in all of the Maya area. Yet it is an anomaly in that it is located on the frontier of the Maya culture area, as opposed to the central core where other great centers like Tikal and Calakmul are found. The site is situated within the Copan Valley, the majority of which was densely settled by the end of the Classic period (Webster and Freter 1990). Although occupation at Copan dates back to the Middle Preclassic period, it does not demonstrate the trappings of Maya culture until the 5th century of the Early Classic period around the time of the foundation of the dynasty (Stuart 2004). New hieroglyphic evidence suggests that the founder of Copan's dynasty, K'inich Yax K'uk Mo', "came from the west" (Stuart 2000, 2004). Although the Teotihuacan style artifacts inside of the tomb believed to belong to Yax K'uk Mo' would suggest the "west" is the Central Mexican site of Teotihuacan, isotopic analysis of the tomb occupant's bones indicate he was in fact from somewhere in the Central Petén (Buikstra, et al. 2004). Through much of the Classic period Copan thrived; the elaborate sculpture, profundity of trade goods, and rapid growth of the population attesting to its power. It appears that the dynasty at Copan not only ruled over the entire Copan valley, but extended its control into the surrounding area. However, in A.D. 738 Quirigua, a possible vassal-site of Copan, captured and "axed" the thirteenth ruler of Copan, an event which may have weakened Copan's strength

(Martin and Grube 2000: 205). By A.D. 820 the royal dynasty collapsed, partially due to a weakened dynasty, a burgeoning class of sub-royal elites, and possibly due to anthropogenic degradation of the surrounding landscape (Fash, et al. 2004).

The wealth of knowledge we possess for Copan is due in large part to the rigorous history of archaeological exploration at the site. Systematic investigations began in 1891 and continued through 1941 as a result of projects from the Peabody Museum of Harvard and the Carnegie Institution of Washington (Gordon 1896; Longyear 1952; Strömsvik 1935). In 1976 and 1977 Gordon Willey of the Peabody Museum directed survey and excavation at Copan, focusing on both excavation of the site core combined with survey and testing of the surrounding valley settlement (Willey 1979). Expanding on the 1970s Peabody Museum work, a series of projects have been conducted at Copan more or less continuously through 2002. These include two Copan Archaeological Projects, PAC I and PAC II, the Rural Sites Project, and the Copan Mosaic Project (Canuto, et al. 2004).

Although Copan boasts one of the largest skeletal samples in the Maya area with approximately 847 individuals (Rhoads 2002: 126), I studied only the skeletons housed at the Peabody Museum of Harvard. These include skeletons collected by the early Peabody Museum and Carnegie investigations as well as individuals recovered from the Peabody's rural settlement survey in the 1970s. As a result, the sample is an interesting mix of burials from the elite core of the site and domestic structures in the hinterland. I collected all of the age and sex data for the Copan skeletons. Since the skeletons from the early investigations are poorly preserved and largely incomplete, the determination of sex and age for many of the Copan skeletons proved difficult. I gathered archaeological context information from Welsh (1988), who compiled the mortuary data for Copan from the Peabody Museum and Carnegie excavations.

Webster and Freter (1990: 55) offer an estimation of 20,000 to 25,000 individuals living in the greater Copan area during the Late Classic period. They employ a rather complex procedure for estimating population at Copan which involves estimating the number of occupied rooms from a count of different types of architecture. In their calculation, they include a structure count increase of 38% for hidden structures, estimate an 80% contemporaneous occupancy, a reduction of 10% for disuse of structures, and an estimate of between 4 and 5 people per room, as well as other minor manipulations. Their final estimate of 20,000 to 25,000 includes rural settlement throughout the Copan Valley and thus is not directly comparable to population estimates for other sites (Webster, personal communication 2004). Rather, a more appropriate area for comparison would be the Copan urban core which they estimate, based on the same methods, to have contained somewhere between 5,797 to 9,464 inhabitants during the height of the Late Classic period (Webster and Freter 1990: 51). The urban core—comprised of the Main Group, Las Sepulturas, and El Bosque—contains a total of 1,071 structures. I use this structure count in my population rank. This estimate reasonably captures Copan's demographic position as a major lowland Maya site, second only to the superpower sites of Tikal and Calakmul.

HIGHLANDS

Kaminaljuyu

Kaminaljuyu is perhaps the single most important site in the Maya highlands. Kaminaljuyu was occupied from the Middle Preclassic through the Late Classic periods. By the Late Preclassic period, the site was one of the largest and most influential sites in the Maya area. At the height of its power, Kaminaljuyu was engaged in a complex network of material and cultural exchange that involved the Maya lowlands, the Guatemalan highlands, the Pacific coast,

and Central Mexico (Braswell 2003). Kaminaljuyu was abandoned in the Late Classic period for reasons yet to be discovered, though Popenoe de Hatch (2001) suspects, based on ceramic evidence, that the event may have involved emigration out of the site. Today much of Kaminaljuyu has been destroyed as a result of the modern expansion of Guatemala City. Early scientific investigations at Kaminaljuyu were conducted by Manuel Gamia, C.A. Villacorta, and J. Antonio Villacorta. From 1935 to 1953, the Carnegie Institution of Washington sponsored a program of archaeological excavation at the site under the direction of Alfred Kidder and Ed Shook (Kidder, et al. 1946). In the 1970s, Pennsylvania State University launched an expedition at Kaminaljuyu under the direction of William Sanders and Joseph Michels (Michels 1979b, c). Since then, the Instituto de Antropología e Historía (INAH) of Guatemala has had several salvage operations at the site, most notably a major project in conjunction with the construction of the modern shopping center, Tikal Futura.

Skeletons from the Carnegie excavations, the Pennsylvania State University excavations, and the INAH salvage projects were used in this study. The majority of the excavations at Kaminaljuyu have focused on the center of the site, thus it is likely that there is a bias for high status individuals in the dental sample. Wright has completed an osteological analysis of some of these skeletons and she kindly provided me with the unpublished data for age and sex. In addition, she compiled all of the mortuary context information which was made available to me.

Michels (1979a: 296) estimates a Late Classic population of 6,500 individuals for Kaminaljuyu. Estimating the number of structures at Kaminaljuyu proved far more difficult than at other sites due to the nature of household construction at the site, much of which is no longer visible. As a result, Michel's (1979a: 287) used an alternative approach to estimate population size at Kaminaljuyu. He based his estimate on the results of test pitting and trenching at the site. Michels assumes a maximum population density in the 7.5 km^2 area of Kaminaljuyu at 21,000

individuals. He then determined what percentage of the landscape was occupied. Since Michels' figure is not based on a structure count, it is necessary to estimate the number of Late Classic residences at Kaminaljuyu using Michel's population estimation. Mayanists use estimates of 4 to 5.6 individuals per house in their population reconstructions (Rice and Culbert 1990). Thus, I use an estimate of 5.0 persons per house at Kaminaljuyu. From this, I extrapolate from Michels' population estimate that there were roughly 1300 structures at Kaminaljuyu. Obviously, this is a very crude estimate considering both the room for error in Michel's original methodology combined with my own overly simplistic approach to estimating the number of structures at Kaminaljuyu. Nonetheless, this estimate seems reasonable considering the relative size and significance of Kaminaljuyu.

PACIFIC COAST

Balberta

Balberta was one of the dominant centers on the Pacific Coast of Guatemala during the Classic period. Although Balberta's roots lie in the Preclassic period, the site reached the apogee of its power during the Early Classic period (Bove 1993). During this time, Balberta consolidated its power to become a fortified center with political control over the surrounding region as a result of military action against its neighbors (Bove and Medrano 2003: 50). There is clear evidence of contact between Balberta and Teotihuacan, although Bove and colleagues believe it was one of mutual interaction and exchange (Bove, et al. 1993).

The site of Balberta is situated on the south coast of Guatemala in the department of Esquintla. The site was first reported by Edwin Shook in 1969. The site was more intensively investigated during the 1980s as part of an archaeological expedition under the direction of Frederick Bove (1993). After preliminary explorations in 1980, Bove began formal work at

Balberta in 1983 in the form of initial surveying and mapping of the site. Formal excavations of Balberta began in 1984, with two intensive field seasons taking place in 1986 and 1987.

A series of 26 burials as well as human remains from non-burial contexts were excavated at Balberta (Arroyo, et al. 1993). Of these, seven individuals were available for study and possessed dental remains. The burials and skeletal remains of Balberta have been extensively studied and served as the subject for two Guatemalan licenciatura theses (Arroyo 1987; Chinchilla 1990). These sources, as well as a more recent summary article on the burials of Balberta (Arroyo, et al. 1993) served as the primary source for burial descriptions and demographic data for the Balberta skeletal series. However, in the original report it was stated that some of the sex estimations were made using burial offerings (Arroyo, et al. 1993: 109). Obviously, this not a reliable means for sex determination, thus all sex estimations are my own. The burials of Balberta date to the Terminal Formative (Late Preclassic) (100 BC – A.D. 200) and the Early Classic (A.D. 200 – 400) periods (Arroyo, et al. 1993). Due to the limitations of sample size for Pacific Coast materials, I included Terminal Formative skeletons in this study.

Actual population estimates are not available for Balberta. However, based on the 26.06 km^2 survey of Balberta, Lou (1993: 33) estimated a maximum population density of 17 persons per km^2. This translates to an estimated population of 443 individuals for the survey area. Considering the size and significance of Balberta, it is likely that this is a conservative estimate. Within this survey area, which includes the bulk of the settlement around Balberta, 111 sites were reported (Lou 1993). Lou indicates that in nearly every case, a site corresponds to a single mound. Thus, there are minimally 111 structures at Balberta.

Montana Complex

The Montana Complex is comprised of a series of major site groups, including Manantial, Loma Linda, and Paraíso, that became incorporated into a single site complex during the Late Classic period. The Montana Complex is perhaps the single most impressive site on the Pacific Coast in terms of architectural construction, including a central core with an 18 m high pyramid atop a giant platform (Bove and Medrano 2003). Based on material evidence, Bove and colleagues argue that, unlike Balberta, the Montana Complex was directly controlled by emissaries and colonizers from Teotihuacan (Bove and Medrano 2003). In fact, it is the success of the Montana Complex with support from Teotihuacan that is believed to have led to the demise of Balberta, perhaps through military conflict (Bove and Medrano 2003: 73).

The Montana Complex was excavated in 1991 and 1992 as part of the Los Chatos-Manantial Project (later renamed the Montana Project) under the direction of Fred Bove (Bove and Medrano 2003). Excavations focused on the architecture of the Los Chatos and Manantial architectural groups, from which the majority of the Montana group skeletons come from. Los Chatos and Manantial are the largest and most impressive of the architectural groups that comprise the Montana Complex.

With the exception of one Early Classic burial, all of the Montana Complex skeletons date to the Late Classic period (Genovez 1997). The majority of the skeletons come from contexts near major ceremonial centers within the Montana complex, suggesting there may be a bias towards higher status individuals in the dental sample. I made all age and sex determinations for the Montana Complex skeletons.

Settlement and population data is presently unavailable for the Montana Complex. However, Bove (2003: 55) indicates that between nuclear zones of Montana and Manantial are

more than 200 mounds. Thus, we can conservatively estimate 200 structures from the Montana complex.

Due to the small sample size for the Pacific Coast, I combined the Balberta and Montana Complex data into a single sample. The result is a sample that is comprised of not only individuals from different sites, but from different time periods. Nonetheless, I feel the pooling of these two is warranted in order to have an outlier sample to compare to the lowlands Maya sites. For this pooled sample, I use a combined structure count of 400 mounds for the purposes of population ranking.

SUMMARY

This chapter detailed the skeletal samples used in this analysis. I analyzed a total of 977 dentitions from 18 sites located across the Maya region. The majority of these individuals date to the Late or Terminal Classic period and are of indeterminate sex. I obtained population estimates from the literature. However, in order to assure comparability of demographic between sites, I chose to use a total structure count, from which the original population estimates were derived, as a means of comparing relative population size between Maya sites.

CHAPTER VI

DENTAL NONMETRIC TRAIT ANALYSES

In this chapter I review the methods and results of my analysis of Classic Maya nonmetric dental variation. The methodology portion of this review includes a discussion of both the data collection and the subsequent statistical analyses. I discuss the implications of those results for ancient Maya population history in Chapter VIII. In the following chapters, I use standard dental anthropological abbreviations for each tooth (Scott and Turner 1997: 25). The first character signifies whether a tooth is from the upper (U) or lower (L) jaw. The second character indicates the tooth class. The third character indicates position, if relevant. For instance, the first maxillary molar is written UM1. Refer to Appendix A for a full list of abbreviations used in this text. Unless otherwise noted, all statistical analyses were performed using SPSS Standard Version 11.5.0.

DATA COLLECTION

In observing and recording dental nonmetric traits, I followed the methodology developed by Christy Turner and colleagues as part of the Arizona State University (ASU) Dental Anthropology System (Turner, et al. 1991). The ASU system is an expanded version of the original data collection protocol for dental morphology developed by Albert Dahlberg (1951; 1956). Turner and colleagues (1991) provide a comprehensive list of traits employed in the ASU system, accompanied by descriptions of the dental traits and advice for properly observing and recording the dental traits. More recently, Scott and Turner (1997) published a comprehensive treatise on the morphology of modern human dentition in which they included expanded descriptions of a majority of the traits in the ASU dental system, as well as numerous

accompanying photographs. In order to further standardize data collection on modern human dental morphology, the ASU Department of Anthropology provides a collection of dental plaques for the dental non-metric traits utilized in the ASU dental system. These casts illustrate the full range of expression of many of the traits scored in the system. I consulted all of these sources extensively throughout the collection of data for this study.

A few of the dental non-metric traits in the ASU dental system are recorded on the basis of presence/absence, such as the odontome of the upper and lower premolars. However, the majority of the traits are scored on a graded expression, from absent to full expression with multiple grades in between. For instance, the Carabelli's cusp of the upper molars can be scored as absent (Grade 0), fully expressed (Grade 7, a large fully formed cusp on the anterior portion of the lingual aspect of crown), or by grades in between which range from slight grooving at the site to free cusps of varying sizes (Grades 1-6) (Turner et al. 1991). The full list of ASU dental traits is provided in Appendix B.

In preparation for collecting the dental trait data, I reviewed the two publications noted above (Scott and Turner 1997; Turner, et al. 1991), as well as other publications which provide descriptions of dental non-metric traits in order to become thoroughly familiarized with the various traits used in this study. I repeatedly consulted these sources throughout the study. In particular, I regularly referred to Turner et al. (1991) during the process of data collection to ensure that the proper grades of each trait were being recorded. I also made continual comparisons with the ASU dental plaques as I scored. I collected all data with the aid of a 10x magnifying lens.

I scored a maximum of 99 tooth-trait combinations for each skeleton. I observed all of the teeth that were present for each individual. However, dental wear, pathology, and missing teeth generally reduced the number of observable traits per individual.

Small sample sizes are often a problem in dental nonmetric studies as a result of missing data due to attrition, ante-mortem and post-mortem tooth loss, etc. Thus, researchers have suggested a number of methods to boost sample sizes in dental nonmetric studies. One approach involves pooling all of the teeth from a series, including antimeres from the same individual, to calculate trait frequencies for that series. Obviously, this method convolutes the genetic structure of a series by allowing some individuals to be represented only once (one antimere observable) and others twice (both antimeres observable) for a given tooth-trait combination.

A more commonly used counting approach is the "individual count" method (Turner 1985c; Turner and Scott 1977). This method attempts to take into consideration bilateral asymmetry of trait expression without over-inflating the sample size. Using the individual count method, when both antimeres of a tooth are present, the trait is counted only once. In cases where the trait is expressed asymmetrically, the maximum expression of the grade is used for statistical analyses. When only one antimere is present, the trait is scored as it appears on that tooth. The underlying assumption of this method is that it is best to score an individual's maximum genetic potential (represented by the largest grade expressed) and that when asymmetry of trait expression does occur, it is random with respect to side (Turner 1985c; Turner and Scott 1977).

Trait Dichotomization

Most statistical analyses of dental nonmetric traits require that the graded dental trait scores be dichotomized into a presence or absence. This involves assigning a breakpoint along the graded scale for each trait to dichotomize the scale into presence/absence. A further benefit of trait dichotomization is a reduction in empty cells in the contingency tables used in nonparametric analyses. Additionally, trait dichotomization reduces intraobserver error by

collapsing the number of observable grades for each trait such that slight discrepancies in scoring of a grade or two are eliminated.

In most dental non-metric studies, researchers use the dichotomization scheme developed by Turner (1986). This scheme is appropriate for examining the variation in trait frequencies between populations around the world. However, this project examines a fairly specific geographic region, wherein most of the populations share a relatively close ancestry. Thus it was desirable to create a dichotomization scheme specific to the Maya area in order to maximize whatever variability might be present. Nichol (1990) is one of few researchers who chose to create his own dichotomization scheme specific for the region he was studying, the American southwest. I follow his methodology to create a trait dichotomization scheme specific for the Maya area.

First, I determined the trait frequency at each grade for each of the sites in the study. Next, I subtracted the minimum site-specific trait frequency for each grade from the maximum frequency of that grade. I then selected whichever grade produced the maximum trait frequency difference between two sites as the breakpoint for that particular trait. I only used sites with samples sizes greater than 20 skeletons (Table 5.1) in this trait dichotomization procedure. The results of the dichotomization are presented in Table 6.1.

Table 6.1. Nonmetric trait dichotomization schemes: Maya area and Turner (1986).

Trait (Grades)	**Tooth**	**Breakpoints (Absent/Present)**	
		(Maya)	*(Turner's)*
Winging (0-3)	UI1	0/1-3	0/1-3
Labial Convexity (0-4)	UI1	0/1-4	0-1/2-4
Shoveling (0-6)	UI1	0-3/4-6	0-2/3-6
Shoveling (0-7)	UI2	0-3/4-7	0-2/3-7
Shoveling (0-6)	UC	0-1/2-6	NA
Double Shoveling (0-6)	UI1	0-4/5-6	0-1/2-6
Double Shoveling (0-6)	UI2	0-3/4-6	0-1/2-6
Double Shoveling (0-6)	UC	0-1/2-6	NA
Double Shoveling (0-6)	UP3	0/1-6	NA
Interruption Groove (0-4)	UI1	0/1-4	0/1-4
Interruption Groove (0-4)	UI2	0/1-4	0/1-4
Tuberculum Dentale (0-6)	UI1	0-1/2-6	0/1-6
Tuberculum Dentale (0-6)	UI2	0-2/3-6	0/1-6
Tuberculum Dentale (0-6)	UC	0-2/3-6	NA
Canine Mesial Ridge (0-3)	UC	0/1-3	0/1-3
Canine Distal Acc. Ridge (0-5)	UC	0-3/4-5	NA
Premolar Acc. Cusp (0-1)	UP3	0/1	0/1
Premolar Acc. Cusp (0-1)	UP4	0/1	0/1
Odontome (0-1)	UP3	0/1	0/1
Odontome (0-1)	UP4	0/1	0/1
Distosagittal Ridge (0-1)	UP3	0/1	0/1
Metacone (0-5)	UM1	0-4/5	NA
Metacone (0-5)	UM2	0-3.5/4-5	0-2/3-5
Metacone (0-5)	UM3	0-3/3.5-5	0-2/3-5
Hypocone (0-5)	UM1	0-4/5	NA
Hypocone (0-5)	UM2	0-3/3.5-5	0-1/2-5
Hypocone (0-5)	UM3	0-1/2-5	0-1/2-5
Metaconule *(Cusp 5)* (0-5)	UM1	0/1-5	0/1-5

Table 6.1. Continued.

Trait (Grades)	**Tooth**	**Breakpoints (Absent/Present)**	
		(Maya)	*(Turner's)*
Metaconule *(Cusp 5)* (0-5)	UM2	0/1-5	NA
Metaconule *(Cusp 5)* (0-5)	UM3	0/1-5	0/1-5
Carabelli's Trait (0-7)	UM1	0-1/2-7	0-4/5-7
Carabelli's Trait (0-7)	UM2	0/1-7	NA
Carabelli's Trait (0-7)	UM3	0/1-7	NA
Parastyle (0-6)	UM1	0/1-6	0/1-6
Parastyle (0-6)	UM2	0/1-6	0/1-6
Parastyle (0-6)	UM3	0/1-6	0/1-6
Enamel Extensions (0-3)	UP3	0/1-3	NA
Enamel Extensions (0-3)	UP4	0/1-3	NA
Enamel Extensions (0-3)	UM1	0/1-3	0/1-3: New World
Enamel Extensions (0-3)	UM2	0-1/2-3	NA
Enamel Extensions (0-3)	UM3	0/1-3	0/1-3: New World
Premolar Root Number (1-2)	UP3	½	1/2
Premolar Root Number (1-2)	UP4	½	NA
Molar Root Number (1-3)	UM1	1-2/3[1]	NA
Molar Root Number (1-3)	UM2	1-2/3	2/3
Molar Root Number (1-3)	UM3	1/2-3	NA
Peg Shaped Incisor (0-2)	UI2	0/1-2	0/1-2
Peg Shaped Molar (0-2)	UM3	0/1-2	0/1-2
Con. Absence, Incisors (0-1)	UI2	0/1	0/1
Con. Absence, Premolars (0-1)	UP4	0/1	NA
Con. Absence, Molars (0-1)	UM3	0/1	0/1
Shoveling (0-3)	LI1/LI2	0-1/2-3	0/1-3
Canine Distal Acc. Ridge (0-5)	LC	0/1-5	NA
Lingual Cusp Variation (0-9)	LP3	0/1-9	NA
Lingual Cusp Variation (0-9)	LP4	0/1-9	0-1/2-9
Odontome (0-1)	LP3	0/1	0/1

Table 6.1. Continued.

Trait (Grades)	**Tooth**	**Breakpoints (Absent/Present)**	
		(Maya)	*(Turner's)*
Odontome (0-1)	LP4	0/1	0/1
Anterior Fovea (0-4)	LM1	0-3/4	NA
Anterior Fovea (0-4)	LM2	0-1/2-4	NA
Anterior Fovea (0-4)	LM3	0/1-4	NA
Groove Pattern (0-2)	LM1	0/1-2 (Y/+, X)	NA
Groove Pattern (0-2)	LM2	0-1/2 (Y,+/X)	0/1-2 (Y/ +, X)
Groove Pattern (0-2)	LM3	0-1/2 (Y,+/X)	NA
Cusp Number (4-6)	LM1	4-5/6	NA
Cusp Number (4-6)	LM2	4/5-6	NA
Cusp Number (4-6)	LM3	4-5/6	NA
Deflecting Wrinkle (0-3)	LM1	0-2/3	0/1-3: New World
Deflecting Wrinkle (0-3)	LM2	0/1-3	NA
Deflecting Wrinkle (0-3)	LM3	0/1-3	NA
Distal Trigonid Crest (0-1)	LM1	0/1	0/1
Distal Trigonid Crest (0-1)	LM2	0/1	NA
Distal Trigonid Crest (0-1)	LM3	0/1	NA
Protostylid (0-7)	LM1	0/1-7	0/1-7
Protostylid (0-7)	LM2	0/1-7	NA
Protostylid (0-7)	LM3	0/1-7	NA
Hypoconulid *(Cusp 5)* (0-5)	LM1	0-4/5	NA
Hypoconulid *(Cusp 5)* (0-5)	LM2	0-1/2-5	0-1/2-5: New World
Hypoconulid *(Cusp 5)* (0-5)	LM3	0/1-5	0-1/2-5: New World
Entoconulid *(Cusp 6)* (0-5)	LM1	0/1-5	0/1-5
Entoconulid *(Cusp 6)* (0-5)	LM2	0/1-5	0/1-5
Entoconulid *(Cusp 6)* (0-5)	LM3	0/1-5	0/1-5
Metaconulid *(Cusp 7)* (0-4)	LM1	0/1-4	0/1-4
Metaconulid *(Cusp 7)* (0-4)	LM2	0/1-4	NA
Metaconulid *(Cusp 7)* (0-4)	LM3	0/1-4	NA

Table 6.1. Continued.

Trait (Grades)	**Tooth**	**Breakpoints (Absent/Present)**	
		(Maya)	*(Turner's)*
Enamel Extensions (0-3)	LP3	0/1-3	NA
Enamel Extensions (0-3)	LP4	0/1-3	NA
Enamel Extensions (0-3)	LM1	0-2/3	0/1-3
Enamel Extensions (0-3)	LM2	0-1/2-3	0/1-3
Enamel Extensions (0-3)	LM3	0-1/2-3	0/1-3
Tome's Root (0-5)	LP3	0-1/2-5	0-2/3-5
Premolar Root Number (1-2)	LP3	½	NA
Premolar Root Number (1-2)	LP4	½	NA
Molar Root Number (1-3)	LM1	1-2/3	1-2/3
Molar Root Number (1-3)	LM2	1/2-3	NA
Molar Root Number (1-3)	LM3	1/2-3	NA
Torsomolar Angle (0-6)	LM3	0/1-6	NA
Congenital Absence (0-1)	LI1	0/1	NA
Congenital Absence (0-1)	LP4	0/1	NA
Congenital Absence (0-1)	LM3	0/1	NA

[1]1-2 Roots treated as a positive expression of the nonmetric trait.

Trait Elimination

Before any statistical analyses could be performed it was necessary to determine if any of the nonmetric traits could potentially introduce error into the analysis. Traits may be problematic if: (1) they could not be replicated reliably from one data collection session to the next, (2) they are affected by the age or sex of the individual, or (3) they were not observable or had a very low fequency in most of the samples.

Intraobserver Error

The assessment of interobserver and intraobserver error is a necessary part of any statistical study employing dental nonmetric traits. However, since I did not use data collected by other researchers, it was not necessary for me to test for interobserver error. Before any statistical analyses can be performed, it is necessary to perform a test of intraobserver error to determine if there was any inconsistency in the collection of nonmetric data over the course of the research project.

In order to test for intraobserver error, I collected duplicate sets of data for 38 individuals from Tikal as well as nine individuals from Altun Ha. The first analysis of the 38 Tikal skeletons took place in June of 1999. These individuals were then re-analyzed during June and July of 2000. The two Altun Ha scoring sessions were separated by a week; the first session occurring at the beginning of my research trip to Trent University in 2003 and the second session at the end of the trip. I combined the Tikal and Altun Ha samples for the analysis of intraobserver error. I assessed intraobserver error following the methodology of Nichol and Turner (1986). I examined interobserver error for all of the traits scored in this analysis with the exception of winging of the upper maxillary incisors since only one skeleton was present in the

sub-sample used for intraobserver analysis. The results of the intraobserver error analysis are presented in Table 6.2.

The first value calculated in the intraobserver analysis is the percentage of traits scored in one session but not in the other (Scored in Only One Session %). Essentially, some traits cannot be reliably assessed even when the tooth is present as a result of attrition, calculus, or some other source of interference. Thus, this value represents the frequency in which I decided a trait was scoreable in one session, but that it was not scoreable in the next. The values in Table 6.2 reveal that this is the most frequent of all intraobserver errors. Values range from 0.0% to 55.6%, with a mean of 24.1%. The most problematic traits are those found on the third molars, as well as enamel extensions. The problematic scoring of third molars is not surprising since they are the most irregular teeth. The error associated with scoring enamel extensions is a little more surprising and is not easily explained. Fortunately, this error statistic does not necessarily indicate a problem in how traits are scored; the remaining statistics deal with this issue.

The next intraobserver error statistic is the percentage of traits that I scored differently between scoring sessions; at any grade level difference (Any Variant Scoring %). Values for this test of error range between 0.0% and 42.9% with a mean of 11.6%. Not surprisingly, the most problematic traits are those with the greatest number of grades (shoveling, Carabelli's cusp, etc.). In general, my values for Any Variant Scoring fall below those of Nichol and Turner (1986), who report a mean of 25.9%. Thus, although there are discrepancies in my choice of when a trait is or is not observable, I am generally consistent in how I score dental traits.

The third statistic calculates the percentage of traits that differed between scoring sessions by more than one grade level difference (> 1 Grade Variant Scoring %). This test of intraobserver error is important since it identifies major discrepancies in grade assessment for

Table 6.2. Analysis of intraobserver concordance (values in bold exceed critical value).

Trait	N Pairs	Scored in only one session %	Variant scoring	>1 Grade variant scoring[1]	Mean grade difference: Absolute %	Mean grade difference: Net[2] %	t (p)[3]
Labial curve UI1	33	24.2	0.0	0.0	0.0	0.0	0.0 (0.00)
Shoveling UI1	35	5.7	8.6	0.0	9.1	-3.0	0.57 (0.57)
Shoveling UI2	27	7.4	33.3	3.7	44.0	36.0	1.22 (0.23)
Shoveling UCR	39	23.1	23.1	0.0	30.0	-16.7	0.33 (0.75)
x2 Shoveling UI1	33	6.1	30.3	6.1	41.9	-29.0	3.24 (0.00)
x2 Shoveling UI2	29	24.1	34.5	3.4	50.0	-22.7	2.08 (0.05)
x2 Shoveling UC	48	29.2	27.1	8.3	61.8	-8.8	1.61 (0.12)
x2 Shoveling UP3	26	46.2	7.7	3.8	21.4	21.4	0.43 (0.67)
Interruption groove UI1	32	0.0	0.0	0.0	0.0	0.0	0.0 (0.00)
Interruption groove UI2	25	16.0	4.0	4.0	14.3	-14.3	1.00 (0.33)
Tuberculum dentale UI1	29	27.6	13.8	0.0	19.0	-9.5	1.00 (0.33)
Tuberculum dentale UI2	18	55.6	16.7	**16.7**	75.0	**75.0**	2.05 (0.08)
Tuberculum dentale UC	35	17.1	42.9	0.0	51.7	3.4	0.25 (0.80)
Mesial ridge UC	34	44.1	0.0	0.0	0.0	0.0	0.0 (0.00)
Distal accessory ridge UC	33	18.2	36.4	6.1	59.3	**44.4**	**2.47 (0.02)**
Accessory cusp UP3	42	19.0	4.8	0.0	5.9	0.0	0.00 (1.00)
Accessory cusp UP4	46	23.9	0.0	0.0	0.0	0.0	0.0 (0.00)
Distalsagittal ridge UP3	54	22.2	0.0	0.0	0.0	0.0	0.0 (0.00)
Metacone UM1	60	3.3	8.3	0.0	8.6	1.7	0.44 (0.66)
Metacone UM2	54	3.7	31.5	0.0	23.1	13.5	1.70 (0.10)
Metacone UM3	26	19.2	30.8	0.0	23.8	-19.0	0.44 (0.67)
Hypocone UM1	58	3.4	27.6	0.0	27.7	9.8	0.77 (0.44)
Hypocone UM2	54	7.4	25.9	0.0	18.0	10.9	1.43 (0.16)
Hypocone UM3	26	30.8	19.2	0.0	25.0	2.8	1.37 (0.19)
Metaconule UM1	46	21.7	2.2	0.0	2.8	-2.8	1.00 (0.32)
Metaconule UM2	49	24.5	2.0	0.0	2.7	2.7	1.00 (0.32)
Metaconule UM3	27	44.4	0.0	0.0	0.0	0.0	0.0 (0.00)
Carabelli's cusp UM1	49	14.3	40.8	6.1	57.1	33.3	1.03 (0.31)
Carabelli's cusp UM2	51	19.6	3.9	0.0	4.9	0.0	0.00 (1.00)
Carabelli's cusp UM3	28	25.0	7.1	7.1	19.0	-19.0	1.45 (0.16)

Table 6.2. Continued.

Trait	N Pairs	Scored in only one session %	Variant scoring %	>1 Grade variant scoring %	Mean grade difference: Absolute %	Mean grade difference: Net %	t (p=)
Paracone UM1	59	15.3	0.0	0.0	0.0	0.0	0.0 (0.00)
Paracone UM2	53	13.2	0.0	0.0	0.0	0.0	0.0 (0.00)
Paracone UM3	29	20.7	0.0	0.0	0.0	0.0	0.0 (0.00)
Enamel extension UP3	41	34.1	0.0	0.0	0.0	0.0	0.0 (0.00)
Enamel extension UP4	47	40.4	0.0	0.0	0.0	0.0	0.0 (0.00)
Enamel extension UM1	34	44.1	20.6	8.8	63.2	**52.6**	1.64 (0.12)
Enamel extension UM2	27	22.2	37.0	0.0	47.6	**19.0**	**2.96 (0.01)**
Enamel extension UM3	15	46.7	20.0	0.0	37.5	**12.5**	0.55 (0.60)
Root number UP1	32	18.8	0.0	0.0	0.0	0.0	0.0 (0.00)
Root number UP2	33	30.3	0.0	0.0	0.0	0.0	0.0 (0.00)
Root number UM1	43	27.9	2.3	0.0	3.2	3.2	1.00 (0.33)
Root number UM2	28	17.9	17.9	0.0	21.7	**21.7**	**2.46 (0.02)**
Root number UM3	22	31.8	0.0	0.0	0.0	0.0	0.0 (0.00)
Peg tooth UI2	34	23.5	2.9	0.0	3.8	3.8	1.00 (0.33)
Peg tooth UM3	29	31.0	0.0	0.0	0.0	0.0	0.0 (0.00)
Odontome UP3	56	25.0	0.0	0.0	0.0	0.0	0.0 (0.00)
Odontome UP4	56	26.8	0.0	0.0	0.0	0.0	0.0 (0.00)
Congenital absence UI2	41	22.0	0.0	0.0	0.0	0.0	0.0 (0.00)
Congenital absence UP3	64	28.1	0.0	0.0	0.0	0.0	0.0 (0.00)
Congenital absence UM3	37	29.7	2.7	0.0	3.8	-3.8	1.00 (0.33)
Lower shoveling LI1	27	22.2	29.6	0.0	38.1	-9.5	.698 (.049)
Distal accessory ridge LC	29	34.5	31.0	**10.3**	68.4	15.8	1.68 (0.11)
Lingual cusp number LP3	41	31.7	12.2	7.3	50.0	**-50.0**	0.71 (0.48)
Lingual cusp number LP4	38	34.2	23.7	2.6	56.0	-24.0	0.60 (0.56)
Anterior fovea LM1	51	15.7	25.5	3.9	34.9	-16.3	1.84 (0.07)
Anterior fovea LM2	48	22.9	25.0	0.0	32.4	-10.8	0.83 (0.41)
Anterior fovea LM3	24	45.8	12.5	0.0	23.1	-7.7	1.00 (0.34)
Groove pattern LM1	62	8.1	19.4	0.0	21.1	3.5	1.16 (0.25)
Groove pattern LM2	61	4.9	13.1	1.6	15.5	8.6	**2.18 (0.03)**
Groove pattern LM3	36	16.7	0.0	0.0	0.0	0.0	0.0 (0.00)
Cusp number LM1	57	17.5	7.0	0.0	8.5	4.3	1.00 (0.32)
Cusp number LM2	42	19.0	11.9	0.0	14.7	2.9	0.44 (0.66)

Table 6.2. Continued.

Trait	N Pairs	Scored in only one session %	Variant scoring %	>1 Grade variant scoring %	Mean grade difference: Absolute %	Mean grade difference: Net %	t (p=)
Cusp number LM3	28	21.4	14.3	3.6	40.9	**-31.8**	0.57 (0.58)
Deflecting wrinkle LM1	61	16.4	24.6	3.3	33.3	2.0	0.65 (0.52)
Deflecting wrinkle LM2	56	16.1	7.1	0.0	8.5	0.0	0.00 (1.00)
Deflecting wrinkle LM3	32	31.3	0.0	0.0	0.0	0.0	0.0 (0.00)
Distal Trigonid Crest LM1	60	21.7	11.7	0.0	14.9	**-14.9**	**2.84** (0.01)
Distal Trigonid Crest LM2	60	23.3	5.0	0.0	6.5	**-6.5**	1.77 (0.08)
Distal Trigonid Crest LM3	29	24.1	3.4	0.0	4.5	-4.5	1.00 (0.33)
Protostylid LM1	58	17.2	15.5	6.9	33.3	-33.3	**2.01** (0.05)
Protostylid LM2	51	27.5	25.5	7.8	56.8	**-35.1**	0.72 (0.47)
Protostylid LM3	30	26.7	13.3	3.3	36.4	-27.3	1.14 (0.27)
Cusp 5 LM1	57	15.8	10.5	0.0	12.5	-4.2	0.00 (1.00)
Cusp 5 LM2	42	21.4	21.4	7.1	51.5	33.3	1.61 (0.12)
Cusp 5 LM3	26	30.8	26.9	**15.4**	88.9	0.0	0.28 (0.79)
Cusp 6 LM1	56	21.4	14.3	0.0	18.2	9.1	0.70 (0.49)
Cusp 6 LM2	42	19.0	11.9	4.8	29.4	-11.8	0.70 (0.49)
Cusp 6 LM3	27	40.7	7.4	0.0	12.5	0.0	0.00 (1.00)
Cusp 7 LM1	60	5.0	1.7	0.0	1.8	1.8	1.00 (0.32)
Cusp 7 LM2	62	11.3	0.0	0.0	0.0	0.0	0.0 (0.00)
Cusp 7 LM3	32	18.8	3.1	3.1	15.4	-15.4	1.00 (0.33)
Enamel extension LP3	30	33.3	0.0	0.0	0.0	0.0	0.0 (0.00)
Enamel extension LP4	35	31.4	0.0	0.0	0.0	0.0	0.0 (0.00)
Enamel extension LM1	34	32.4	26.5	5.9	47.8	-4.3	0.77 (0.45)
Enamel extension LM2	36	33.3	22.2	0.0	33.3	8.3	**2.30** (0.03)
Enamel extension LM3	16	31.3	18.8	6.3	36.4	**-18.2**	0.80 (0.44)
Tomes' root LP3	17	52.9	23.5	**17.6**	47.5	**-77.5**	0.81 (0.44)
Root number LP3	28	25.0	3.6	3.6	14.3	**14.3**	1.00 (0.33)
Root number LP4	29	6.9	0.0	0.0	0.0	0.0	0.0 (0.00)
Root number LM1	37	29.7	0.0	0.0	0.0	0.0	0.0 (0.00)
Root number LM2	33	21.2	6.1	0.0	7.7	7.7	0.00 (1.00)
Root number LM3	14	28.6	14.3	0.0	20.0	**-20.0**	1.50 (0.17)
Odontome LP3	43	37.2	2.3	0.0	3.7	-3.7	0.0 (0.00)
Odontome LP4	41	31.7	4.9	0.0	7.1	7.1	1.44 (0.16)

Table 6.2. Continued.

Trait	N Pairs	Scored in only one session %	Variant scoring %	>1 Grade variant scoring %	Mean grade difference: Absolute %	Mean grade difference: Net %	t (p=)	Trait
Torsomolar LM3	9	11.1	0.0	0.0	0.0	0.0	0.0	(0.00)
Congenital absence LI1	40	50.0	0.0	0.0	0.0	0.0	0.0	(0.00)
Congenital absence LP3	56	23.2	0.0	0.0	0.0	0.0	0.0	(0.00)
Congenital absence LM3	40	25.0	0.0	0.0	0.0	0.0	0.0	(0.00)

[1]Critical value is 10.0%.
[2]Critical value is the largest grade for each respective trait multiplied by 5%.
[3]Critical value is $p < .05$.

dental traits. Typically, trait dichotomization will eliminate any error that may result from a difference of only one grade (see the previous section), but if the discrepancy is consistently greater the trait may be problematic. My values for >1 Grade Variant Scoring range from 0.0% to 17.6% with a mean of only 1.9%. Overall, this indicates substantial consistency between the scoring sessions and suggests that when discrepancies are made, they are only of one grade. These values are lower than those reported by Nichol and Turner (1986), who found a mean of 5.6% in their study. Nichol and Turner (1986) propose a critical value of 10% for this test of intraobserver error. In this study, four traits exceed the critical value: tuberculum dentale (UI2), distal accessory ridge (LC), Tome's root (LP3), and cusp 5 (LP3).

The fourth statistic calculated is the Absolute Mean Grade Difference % (AMGD). This index measures the mean grade difference between the first and the second scoring sessions for a given trait. This index does not take into account the directionality of the scoring difference—was a trait consistently scored at higher or lower grade between sessions? The formula for the calculation of this index is

$$AMGD = \frac{\Sigma(|x_2 - x_1|)}{n} \times 100$$

where x_2 is the grade number assigned to the trait during the second scoring session, x_1 is the grade number assigned to the trait during the first scoring session, and n is the number of individuals that could be scored for that trait between the two scoring sessions. My results for this value range from 0.0% to 88.9% with a mean value of 20.0%. In other words, for the average individual for the average trait, a 1/5 grade error is being made. Again, my values fall below those of Nichol and Turner (1986) who report a mean AMGD of 32.0%.

The fifth value is the Net Mean Grade Difference % (NMGD). This index is similar to the AMGD in that it measures the mean grade difference between the first and the second scoring session for a given trait. Unlike the AMGD however, the NMGD takes into account the directionality of the scoring difference such that negative NMGDs suggest that during the first session a particular trait was generally scored at a higher grade, whereas a positive NMGD suggests the reverse. The formula for the NMGD is

$$NMGD = \frac{\Sigma(x_2 - x_1)}{n} \times 100$$

with the variables as defined above. My results for the NMGD range between -50.0% and 75% with a mean of -0.5%. In other words some traits did show directionality in their error between tests, though the majority did not. The cases of directionality suggest consistent errors between scoring sessions. For example, for a given trait, I might have consistently scored a grade 1 in the first scoring session and a grade 2 in the next. Nichol and Turner consider NMGD values critical when the NMGD exceeds the maximum grade of the trait multiplied by .05. Fifteen traits exceed the critical value: tuberculum dentale (UI2), distal accessory ridge (UC), lingual cusp number (LP3), cusp number (LM3), distal trigonid crest (LM1, LM2), protostylid (LM2), enamel extension (UM1, UM2, UM3, LM3), Tomes' root (LP3), and root number (UM2, LP3, LM3).

The final value calculated is a paired sample Student's *t*-test. When using the *t*-test, it is recommended that all classification grades be spaced equally (Nichol and Turner 1986). Thus, in the case of the metacone and the hypocone I rounded any scores of 3.5 up to 4 or down to 3, based on the grade scored in the other scoring session such that any difference in grade between sessions would be maintained. For example, if I scored a grade of 4 in the first session and 3.5 in the second, I would treat the score from second session as grade 3. Nichol and Turner (1986) consider traits problematic if the *t*-test is significant at the .05 level. In this study the following

traits have a significance value of $p < .05$: distal accessory ridge (UC), enamel extension (UM2), root number (UM2), groove pattern (LM2), distal trigonid crest (LM1).

I follow Nichol and Turner's (1986: 302) recommendation that traits are problematic if they exceed the critical value for two or more of the following tests: > 1 Grade Variant Scoring, NMGD, or the paired sample *t*-test. The following traits meet these criteria: tuberculum dentale (UI2), distal accessory ridge (UC), Enamel extension (UM2), Root number (UM2), Distal Trigonid Crest (LM1), Tomes' root (LP3). I eliminated these traits from all of the multivariate analyses that follow.

Sex Effects on Nonmetric Traits

Most researchers who use the ASU dental anthropology system pool sexes for statistical analysis, under the assumption that very little sexual dimorphism is exhibited in the dentition of modern humans (Scott and Turner 1997). Nonetheless, some researchers have found an association between sex and select nonmetric traits in their studies (Nichol 1990; Powell 1995; Rhoads 2002). I have chosen to identify those traits that are associated with sex and remove them so that I can justifiably pool the sexes for further statistical analyses. This is important to ensure the largest sample size possible.

A chi-square analysis was performed to identify traits that demonstrate differences by sex. For this analysis, I pooled the entire sample and used dichotomized trait frequencies. In some cases, the chi-square analysis could not be performed because one of the cells in the contingency table had an expected count of less than five. However, these are generally the same traits that are uncommon throughout the Maya dental series and thus would be excluded on those grounds as well. The traits excluded by this due to low sample size are: winging (UI1), labial curve (UI1), canine mesial ridge (UC), premolar accessory cusp (UP3, UP4), distosagittal

ridge (UP3), odontome (UP3, UP4, LP3, LP4), metaconule (UM1, UM2, UM3), Carabelli's cusp (UM3), parastyle (UM1, UM2, UM3), deflecting wrinkle (LM2, LM3), distal trigonid (LM1, LM2, LM3), metaconulid (LM2, LM3), enamel extension (UP3, UP4, LP3, LP4), root number (UP4, UM1, LP3, LP4, LM1), torsomolar angle (LM3), and congenital absence (UI2, UP4, UM3, LI1, LP3). Traits are considered to have an association with sex when their *p*-value is less than .05. Performing repeated chi-square tests significantly increases the likelihood of familywise error—where some traits may demonstrate an association with sex even when they are not associated in reality. However, I feel this acceptable in light of the need to be conservative in removing any traits that might exhibit an association with sex. Traits with a demonstrated association with sex are presented in Table 6.3

Rare Nonmetric Traits/Low Sample Size

As already noted, a number of dental traits rarely occurred among the ancient Maya samples scored in this study. For biological distance statistics like the Mean Measure of Divergence, rare traits are problematic because their frequencies inevitably do not vary between samples and thus exaggerate the similarities between the samples (Sjøvold 1973). Thus, I eliminated all rare traits from statistical analyses. In addition, I removed traits with low sample sizes. For the Mean Measure of Divergence (see below), generally, a sample size of ten observations for each site per trait are required (Irish 1993). Finally, Turner and colleagues recommend using a single, or "key", tooth for each trait in multivariate analyses (Scott and Turner 1997; Turner, et al. 1991) because the phenotypic expression of a trait in each of the different teeth of the same class may be controlled by the same suite of genes. Generally, the key tooth is the tooth that is most variable for a given trait. In many cases it is the polar tooth, though not always, and third molars are rarely used due to their highly irregular

Table 6.3. Traits that demonstrate an association with sex based on Chi-square analysis.

Trait	χ^2	***p*-value**
Carabelli's cusp (UM1)	4.753	.029
Enamel extension (UM1)	5.760	.016
Root number (UM2)	8.657	.003
Root number (UM3)	6.876	.009
Peg shaped molar (UM3)	9.803	.002

nature. Limiting traits to key teeth avoids the risk of weighting certain traits in the analysis. When possible, I followed Turner and colleague's key tooth recommendations. However, in some instances I chose a non-key tooth if that tooth presented a preferable sample size. For molars, I consider only first or second molars. Table 6.4 lists the final suite of traits excluded and included in the multivariate analyses.

STATISTICAL METHODS

I have selected a variety of univariate and multivariate statistical approaches for analyzing population variability with dental nonmetric data. Unlike metric data, nonmetric data are not readily analyzed with current model-bound statistical methods. Thus all of the statistical approaches discussed here are considered model-free following the nomenclature outlined in Chapter IV.

Likelihood Ratio

I used a likelihood ratio (G^2) to identify traits that vary significantly between sites. I included only sites that consistently possessed sample sizes larger than 10 for each trait. The test was performed on the dichotomized data for each trait listed in Table 6.4. Traits were also excluded that had contingency tables with more than 20% of cells having expected values less than five. All p-values were adjusted for familywise error using Šidák single-step method: $p = 1-(1-p_i)^k$ where p_i is the original p-value for trait i and k is the total number of likelihood ratio tests performed (Westfall and Young 1993). The results of the likelihood ratio aided in the selection of traits that I used for multivariate analyses.

Table 6.4. Nonmetric dental traits included and excluded from statistical analyses.

Trait	EXCLUDED			INCLUDED
	Intraobserver error	Sex Effect	Small sample/Low Variability/Non-Key Tooth	
Winging (UI1)			X	
Labial Convexity (UI1)			X	
Shoveling (UI1)				X
Shoveling (UI2)			X	
Shoveling (UC)				X
Double Shoveling (UI1)				X
Double Shoveling (UI2)			X	
Double Shoveling (UC)				X
Double Shoveling (UP3)			X	
Int. Groove (UI1)			X	
Int. Groove (UI2)				X
Tub. Dentale (UI1)				X
Tub. Dental (UI2)			X	
Tub. Dentale (UC)				X
Distal Acc. Ridge (UC)	X			
Mesial Ridge (UC)			X	
Accessory Cusp (UP3)			X	
Accessory Cusp (UP4)			X	
Distosagittal Ridge			X	
Metacone (UM1)			X	
Metacone (UM2)				X
Metacone (UM3)			X	
Hypocone (UM1)				X
Hypocone (UM2)			X	
Hypocone (UM3)			X	
Metaconule (UM1)			X	
Metaconule (UM2)			X	
Metaconule (UM3)			X	

Table 6.4. Continued.

Trait	EXCLUDED			INCLUDED
	Intraobserver error	**Sex Effect**	**Small sample/Low Variability/Non-Key Tooth**	
Carabelli's Cusp (UM1)		X		
Carabelli's Cusp (UM2)			X	
Carabelli's Cusp (UM3)			X	
Parastyle (UM1)			X	
Parastyle (UM2)			X	
Parastyle (UM3)			X	
Enamel Ext. (UP3)			X	
Enamel Ext. (UP4)			X	
Enamel Ext. (UM1)		X		
Enamel Ext. (UM2)	X			
Enamel Ext. (UM3)			X	
Odontome (UP3)			X	
Odontome (UP4)			X	
Root Number (UP3)			X	
Root Number (UP4)			X	
Root Number (UM1)			X	
Root Number (UM2)	X	X		
Root Number (UM3)		X		
Peg Incisor (UI2)				X
Peg Molar (UM3)		X		
Congenital Abs. (UI2)			X	
Congenital Abs. (UP4)			X	
Congenital Abs. (UM3)				X
Lower Shoveling (UI1)			X	
Distal Acc. Ridge (LC)			X	
Premolar Cusp # (LP3)				X
Premolar Cusp # (LP4)			X	
Anterior Fovea (LM1)				X

Table 6.4. Continued.

Trait	EXCLUDED			INCLUDED
	Intraobserver error	**Sex Effect**	**Small sample/Low Variability/Non-Key Tooth**	
Anterior Fovea (LM2)			X	
Anterior Fovea (LM3)			X	
Groove Pattern (LM1)				X
Groove Pattern (LM2)			X	
Groove Pattern (LM3)			X	
Cusp Number (LM1)			X	
Cusp Number (LM2)				X
Cusp Number (LM3)			X	
Def. Wrinkle (LM1)				X
Def. Wrinkle (LM2)			X	
Def. Wrinkle (LM3)			X	
Distal Tri. Crest (LM1)	X		X	
Distal Tri. Crest (LM2)			X	
Distal Tri. Crest (LM3)			X	
Protostylid (LM1)			X	
Protostylid (LM2)				X
Protostylid (LM3)			X	
Hypoconulid (LM1)				X
Hypoconulid (LM2)			X	
Hypoconulid (LM3)			X	
Entoconulid (LM1)				X
Entoconulid (LM2)			X	
Entoconulid (LM3)			X	
Metaconulid (LM1)				X
Metaconulid (LM2)			X	
Metaconulid (LM3)			X	
Tomes' root (LP3)	X			
Odontome (LP3)			X	

Table 6.4. Continued.

	EXCLUDED			INCLUDED
Trait	**Intraobserver error**	**Sex Effect**	**Small sample/Low Variability**	
Odontome (LP4)				X
Enamel Ext. (LP3)			X	
Enamel Ext. (LP4)			X	
Enamel Ext. (LM1)				X
Enamel Ext. (LM2)			X	
Enamel Ext. (LM3)			X	
Root Number (LP3)			X	
Root Number (LP4)			X	
Root Number (LM1)			X	
Root Number (LM2)			X	
Root Number (LM3)			X	
Torsomolar angle (LM3)			X	
Congenital Abs. (LI1)			X	
Congenital Abs. (LP3)			X	
Congenital Abs. (LM3)				X

Mean Measure of Divergence

The accepted statistical method of choice for nonmetric (dental and cranial) biological distance studies is C.A.B. Smith's Mean Measure of Divergence (MMD). Berry and Berry (1967) were among the first researchers to employ the MMD to explore biological affinities in human populations. The formula they suggested is the most commonly used. Before dichotomized trait frequencies can be used in the MMD, they must undergo an angular transformation to stabilize the variance of unequal sample sizes. Green and Suchey (1976) analyzed the Grewal-Smith transformation utilized by Berry and Berry (1967) as well as a number of other angular transformations designed to control for small sample sizes. They recommend that the Freeman-Tukey (1950) transformation be used. In addition, Green and Suchey (1976) proposed minor modifications to the MMD statistic. The recommendations of Green and Suchey (1976) are currently followed by the vast majority of researchers utilizing the MMD statistic, and are used in this study. Their formula for the MMD is

$$MMD = \sum_{i=1}^{r} \frac{(\theta_{1i} - \theta_{2i})^2 - (\frac{1}{n_{1i} + .5} + \frac{1}{n_{2i} + .5})}{r}$$

where r is the number of traits considered, θ_{1i} is the angular transformation of the frequency of the ith trait in the first sample, θ_{2i} is the angular transformation of the frequency of the ith trait in the second sample, n_{1i} is the number of individuals in the first sample observed for trait i, and n_{2i} is the number of individuals in the second sample observed for trait i.

As proposed by Green and Suchey (1976), the Freeman-Tukey angular transformation is

$$\theta = \tfrac{1}{2}\sin^{-1}\left(1 - \frac{2k}{n+1}\right) + \tfrac{1}{2}\sin^{-1}\left(1 - \frac{2(k+1)}{n+1}\right)$$

where k_{ji} is the number of individuals in sample j classified for trait i, n_{ji} is, as defined above, the number of individuals in sample j observable for trait i. It should be noted that the angular

transformation is calculated in radians, not degrees. The Freeman-Tukey angular transformation has been demonstrated to reliably stabilize variance when sample sizes are greater than 10 for each trait for each site in the analysis (Green and Suchey 1976).

In order to calculate the variance of the MMD, Sjøvold (1973) proposed the following formula:

$$VAR_{MMD} = \frac{2}{r^2}\sum_{i=1}^{r}\left(\frac{1}{n_{1i}+.5}+\frac{1}{n_{2i}+.5}\right)^2.$$

The standard deviation of the MMD is thus:

$$sd_{MMD} = \sqrt{VAR_{MMD}}.$$

In order to test the significance of the MMD, Sjøvold (1973) demonstrated that a MMD was significant if it exceeded twice its standard deviation. According to Sjøvold, this test has a 0.05 level of significance. However, Green and Suchey (1976) suggest that the significance level of this test is actually 0.03.

Some authors (Hemphill, et al. 1991; Prowse and Lovell 1996; Sofaer, et al. 1986) recommend using standardized MMD values when sample sizes vary between series. Standardized MMD values are calculated by dividing the raw MMD values by its standard deviation. Sjøvold (1973) indicates that standardized MMD values greater than 2.0 are significant at the .05 probability level.

Cluster Analysis

In order to better visualize the pairwise distance values that result from running the MMD statistic, I used cluster analysis. Cluster analysis is the most commonly used method for displaying biological distances based on non-metric data. Several techniques exist for running cluster analyses. I selected Ward's Method of hierarchical agglomeration for this study,

primarily because it is a technique that has proven reliable in past biological distance studies (Irish 1993). In cluster analysis, MMD values are reconfigured into squared Euclidian distances, which are then used in creating the clusters. In this approach, each sample begins as a separate cluster and joining proceeds until every sample is amalgamated. Ward's Method creates clusters that minimize within-cluster variability (Baxter 1994). Any joining increases that variability, thus clustering proceeds in an order that produces clusters with the least amount of variability increase. In Ward's Method, the point of cluster linkage is based on a Sum of Squares.

Resulting clusters are presented in dendograms, with each branch representing a separate clustering event. Caution must be exercised in interpreting cluster analysis dendograms. Because the dendograms resemble family trees, researchers have had a tendency to interpret them as a 1 to 1 reconstruction of population history, with each branch in the dendogram representing actual biological fissioning events. In reality, any reconstruction of population history is far more complex, resulting from the complex interplay of genetic isolation, migration, and genetic drift. Thus, the dendograms are useful tools for identifying population similarity, but are not direct reconstructions of population history.

Multidimensional Scaling

As an alternative to the cluster analysis, I used multidimensional scaling. Multidimensional scaling plots groups based on distance matrices (i.e. the MMD matrix). As the name of the technique implies, a number of dimensions can be used to present the data, however, I selected only two-dimensions as they are far easier to read and interpret than three dimensional plots.

RESULTS

The dichotomized dental trait frequencies for Classic period Maya sites are presented in Table 6.5. A majority of the traits exhibit moderate frequencies across the Maya samples. This is partly due to the Maya-specific dichotomization scheme that I designed to maximize dental trait variability in the samples studied. However, a number of traits are common amongst most of the samples, such as the tuberculum dentale (UI1, UI3, UC), metacone (UM2), and Carabelli's cusp (UM1). Similarly, a number of traits are rare among the series considered, such as labial curve (UI1), canine mesial ridge (UC), distal sagittal ridge (UC), parastyle (UM1), distal trigonid crest (LM1), and metaconulid (LM1). I anticipated these findings because many of these trait frequency patterns are characteristic of New World populations (Scott and Turner 1997; Turner 1985b; C. G. Turner, II 1990). However, it is important to underscore that the data presented here are not directly comparable to those presented elsewhere due to the unique dichotomization scheme I used (Table 6.1). For instance, shoveling (UI1) occurs at relatively low to moderate frequencies here whereas in most other studies of New World populations, the trait occurs at higher frequencies. This is because the dichotomization point in this study was set at grade 3, whereas in Turner's work, it was set to grade 2. When compared to the studies of Maya populations by Jacobi (1996), Rhoads (2002), and Wrobel (2003), the frequencies presented here are generally similar. However, direct comparisons are not possible, since these studies all used Turner's (1986) dichotomization scheme.

Table 6.5. Dichotomized Classic period dental trait frequencies.

SITE	Winging (UI1)		Labial Curve (UI1)		Shoveling (UI1)[1]		Shoveling (UI2)		Shoveling (UC)	
CENTRAL ZONE										
Tikal	0/3	(0.0%)	10/72	(13.9)	21/91	(23.1%)	49/92	(53.3%)	20/107	(18.7%)
Tikal: Caches & Pr. Dep.	1/1	(100%)	1/14	(7.1)	2/17	(11.8%)	8/17	(47.1%)	3/14	(21.4%)
Uaxactun	1/1	(100%)	1/5	(20.0)	1/5	(20.0)	3/4	(75.0%)	1/6	(16.7%)
Calakmul	1/1	(100%)	0/14	(0.0)	7/23	(30.4)	15/20	(75.0%)	0/17	(0.0%)
USUMACINTA ZONE										
Piedras Negras	----	----	2/40	(5.0%)	7/49	(14.3%)	15/37	(40.5%)	15/34	(44.1%)
PASIÓN ZONE										
Altar de Sacrificios	0/2	(0.0%)	2/17	(11.8%)	9/17	(52.9%)	13/25	(52.0%)	4/19	(21.1%)
Seibal	----	----	2/9	(22.2%)	7/16	(43.8%)	9/15	(60.0%)	3/14	(21.4%)
Dos Pilas	----	----	2/12	(16.7%)	5/29	(17.2%)	24/30	(80.0%)	5/31	(16.1%)
Aguateca	----	----	2/6	(33.3%)	2/5	(40.0%)	6/9	(66.7%)	1/6	(16.7%)
Tamarindito	----	----	0/4	(0.0%)	1/8	(12.5%)	7/7	(100.0%)	3/6	(50.0%)
Itzán	----	----	0/2	(0.0%)	0/2	(0.0%)	0/3	(0.0%)	0/4	(0.0%)
BELIZE ZONE										
Altun Ha	1/1	(100.0%)	3/26	(11.5%)	7/40	(17.5%)	18/40	(45.0%)	4/41	(9.8%)
Barton Ramie	----	----	3/13	(23.1%)	1/18	(5.6%)	7/18	(38.9%)	1/14	(7.1%)
Baking Pot	----	----	0/2	(0.0%)	1/2	(50.0%)	3/5	(60.0%)	0/4	(0.0%)
Colha	1/1	(100.0%)	1/13	(7.7%)	4/18	(22.2%)	7/13	(53.8%)	4/7	(57.1%)
SOUTHWESTERN ZONE										
Copan	----	-----	3/8	(37.5%)	9/19	(47.4%)	7/10	(70.0%)	0/7	(0.0%)
HIGHLANDS ZONE										
Kaminaljuyu	----	-----	0/9	(0.0%)	3/11	(27.3%)	6/10	(60.0%)	4/14	(28.6%)
PACIFIC COAST ZONE										
Balberta	----	-----	0/1	(0.0%)	1/2	(50.0%)	1/2	(50.0%)	0/1	(0.0%)
Montana Complex	0/1	(0.0%)	0/3	(0.0%)	2/6	(33.3%)	4/7	(57.1%)	1/5	(20.0%)
COMBINED SAMPLE	5/11	(45.5%)	32/270	(11.9%)	90/378	(23.8%)	202/364	(55.5%)	69/351	(19.7%)

Table 6.5. Continued.

SITE	x2 Shoveling (UI1)		x2 Shoveling (UI2)		x2 Shoveling (UC)		x2 Shoveling (UP3)		Int. Groove (UI1)	
CENTRAL ZONE										
Tikal	29/81	(35.8%)	13/69	(17.8%)	29/97	(29.9%)	36/53	(67.9%)	5/78	(6.4%)
Tikal: Caches & Pr. Dep.	6/16	(35.8%)	2/10	(20.0%)	0/13	(0.0%)	13/15	(86.7%)	1/12	(8.3%)
Uaxactun	1/5	(20.0%)	0/2	(0.0%)	0/5	(0.0%)	4/6	(66.7%)	0/2	(0.0%)
Calakmul	9/16	(56.3%)	6/13	(46.2%)	3/21	(14.3%)	17/26	(65.4%)	4/21	(19.0%)
USUMACINTA ZONE										
Piedras Negras	10/42	(23.8%)	6/30	(20.0%)	22/54	(40.7%)	11/17	(64.7%)	7/46	(15.2%)
PASIÓN ZONE										
Altar de Sacrificios	3/16	(18.8%)	1/17	(5.9%)	1/23	(4.3%)	20/25	(80.0%)	0/17	(9.1%)
Seibal	2/9	(22.2%)	1/14	(7.1%)	2/14	(14.3%)	13/19	(68.4%)	1/20	(0.0%)
Dos Pilas	5/17	(29.4%)	2/10	(20.0%)	12/30	(40.0%)	20/30	(66.7%)	2/27	(7.4%)
Aguateca	2/5	(40.0%)	2/7	(28.6%)	5/7	(71.4%)	5/6	(83.3%)	1/6	(16.7%)
Tamarindito	2/5	(40.0%)	0/3	(0.0%)	3/6	(50.0%)	4/6	(66.7%)	1/6	(16.7%)
Itzán	0/2	(0.0%)	1/2	(50.0%)	0/3	(0.0%)	1/3	(33.3%)	0/2	(0.0%)
BELIZE ZONE										
Altun Ha	6/37	(16.2%)	3/30	(10.0%)	5/44	(11.4%)	29/43	(67.4%)	7/28	(25.0%)
Barton Ramie	4/17	(23.5%)	3/15	(20.0%)	2/18	(11.1%)	10/24	(50.0%)	0/21	(0.0%)
Baking Pot	1/2	(50.0%)	1/2	(50.0%)	0/5	(0.0%)	4/5	(80.0%)	0/1	(0.0%)
Colha	6/17	(35.3%)	1/8	(12.5%)	4/7	(57.1%)	2/4	(50.0%)	2/13	(15.4%)
SOUTHWESTERN ZONE										
Copan	2/7	(28.6%)	0/3	(0.0%)	0/10	(0.0%)	20/28	(71.4%)	2/12	(16.7%)
HIGHLANDS ZONE										
Kaminaljuyu	3/8	(37.5%)	2/8	(25.0%)	2/14	(14.3%)	10/12	(83.3%)	1/7	(14.3%)
PACIFIC COAST ZONE										
Balberta	0/2	(0.0%)	0/2	(0.0%)	0/2	(0.0%)	1/1	(100.0%)	0/2	(0.0%)
Montana Complex	4/5	(80.0%)	2/4	(50.0%)	0/4	(0.0%)	2/4	(50.0%)	0/7	(0.0%)
COMBINED SAMPLE	95/309	(30.7%)	46/249	(18.5%)	90/377	(23.9%)	222/323	(68.7%)	34/314	10.8%)

Table 6.5. Continued.

SITE	Int. Groove (UI2)		Tub. Dentale (UI1)		Tub. Dentale (UI2)		Tub. Dentale (UC)		Mesial Ridge (UC)	
CENTRAL ZONE										
Tikal	19/74	(25.7%)	32/69	(46.4%)	27/57	(47.4%)	55/95	(57.9%)	2/76	(2.6%)
Tikal: Caches & Pr. Dep.	5/9	(55.6%)	12/16	(75.0%)	10/12	(83.3%)	10/11	(90.9%)	1/8	(12.5%)
Uaxactun	1/3	(33.3%)	2/3	(66.7%)	1/1	(100.0%)	2/5	(40.0%)	0/4	(0.0%)
Calakmul	3/16	(18.8%)	9/16	(56.3%)	6/13	(46.2%)	14/20	(70.0%)	0/18	(0.0%)
USUMACINTA ZONE										
Piedras Negras	17/32	(53.1%)	17/29	(58.6%)	8/24	(33.3%)	11/33	(33.3%)	2/22	(9.1%)
PASIÓN ZONE										
Altar de Sacrificios	8/20	(40.0%)	1/10	(10.0%)	6/13	(46.2%)	15/20	(75.0%)	0/15	(0.0%)
Seibal	3/14	(21.4%)	2/12	(16.7%)	2/12	(16.7%)	10/12	(83.3%)	2/8	(25.0%)
Dos Pilas	10/21	(47.6%)	9/21	(42.9%)	12/20	(60.0%)	14/36	(38.9%)	2/20	(10.0%)
Aguateca	4/9	(44.4%)	2/4	(50.0%)	1/5	(20.0%)	1/5	(20.0%)	1/4	(25.0%)
Tamarindito	2/5	(40.0%)	2/5	(40.0%)	1/3	(33.3%)	6/8	(75.0%)	0/5	(0.0%)
Itzán	2/3	(66.7%)	2/3	(66.7%)	1/1	(100.0%)	2/3	(33.3%)	0/1	(0.0%)
BELIZE ZONE										
Altun Ha	13/24	(54.2%)	25/34	(73.5%)	18/22	(81.8%)	31/45	(68.9%)	2/32	(6.3%)
Barton Ramie	5/14	(35.7%)	7/18	(38.9%)	8/13	(66.5%)	8/15	(53.3%)	4/11	(36.4%)
Baking Pot	2/4	(50.0%)	-----	-----	1/1	(100.0%)	4/4	(100.0%)	0/3	(0.0%)
Colha	2/7	(28.6%)	8/13	(61.5%)	4/9	(66.7%)	2/8	(25.0%)	0/5	(0.0%)
SOUTHWESTERN ZONE										
Copan	1/8	(12.5%)	4/9	(44.4%)	3/6	(50.0%)	6/10	(60.0%)	0/7	(0.0%)
HIGHLANDS ZONE										
Kaminaljuyu	1/7	(14.3%)	6/8	(75.0%)	4/6	(66.7%)	12/15	(80.0%)	2/11	(18.2%)
PACIFIC COAST ZONE										
Balberta	0/2	(0.0%)	0/2	(0.0%)	0/1	(0.0%)	1/1	(100.0%)	0/1	(0.0%)
Montana Complex	7/7	(100.0%)	5/6	(83.3%)	2/5	(40.0%)	2/4	(50.0%)	0/3	(0.0%)
COMBINED SAMPLE	105/279	(37.6%)	145/278	(52.2%)	115/224	51.3%)	206/350	(58.9%)	18/254	(7.1%)

Table 6.5. Continued.

SITE	D.A. Ridge (UC)		Acc. Cusp (UP3)		Acc. Cusp (UP4)		DistSa. Ridge (UP3)		Metacone (UM1)	
CENTRAL ZONE										
Tikal	29/57	(50.9%)	7/104	(7.1%)	5/93	(5.4%)	0/117	(0.0%)	123/142	(86.6%)
Tikal: Caches & Pr. Dep.	5/8	(62.5%)	2/11	(18.2%)	1/10	(10.0%)	0/17	(0.0%)	19/21	(90.5%)
Uaxactun	0/1	(0.0%)	0/7	(0.0%)	0/5	(0.0%)	1/7	14.3	5/7	(71.4%)
Calakmul	9/11	(81.8%)	3/16	(18.8%)	3/18	(16.7%)	0/25	(0.0%)	24/29	(82.8%)
USUMACINTA ZONE										
Piedras Negras	3/9	(16.7%)	1/30	(3.3%)	1/31	(3.2%)	0/43	(0.0%)	48/55	(87.3%)
PASIÓN ZONE										
Altar de Sacrificios	4/10	(33.3%)	2/20	(10.0%)	1/13	(7.7%)	0/23	(0.0%)	26/31	(83.9%)
Seibal	4/5	(80.0%)	0/15	(0.0%)	0/15	(0.0%)	0/21	(0.0%)	15/23	(65.2%)
Dos Pilas	7/14	(50.0%)	1/35	(2.9%)	1/35	(2.9%)	0/42	(0.0%)	33/40	(82.5%)
Aguateca	1/2	(50.0%)	0/9	(0.0%)	0/7	(0.0%)	1/10	10.0	9/9	(100.0%)
Tamarindito	3/3	(100.0%)	1/10	(10.0%)	0/8	(0.0%)	0/4	(0.0%)	6/7	(85.7%)
Itzán	2/2	(100.0%)	1/4	(25.0%)	0/4	(0.0%)	0/4	(0.0%)	3/3	(100.0%)
BELIZE ZONE										
Altun Ha	10/30	(33.3%)	3/27	(11.1%)	3/23	(13.0%)	0/41	(0.0%)	54/64	(84.4%)
Barton Ramie	3/8	(37.5%)	2/15	(13.3%)	0/12	(0.0%)	1/17	5.0	13/20	(65.0%)
Baking Pot	1/1	(100.0%)	0/4	(0.0%)	0/2	(0.0%)	0/5	(0.0%)	8/9	(88.9%)
Colha	4/8	(50.0%)	0/16	(0.0%)	0/10	(0.0%)	0/17	(0.0%)	13/21	(61.9%)
SOUTHWESTERN ZONE										
Copan	3/6	(50.0%)	3/17	(17.6%)	0/8	(0.0%)	0/18	(0.0%)	26/32	(81.3%)
HIGHLANDS ZONE										
Kaminaljuyu	6/13	(46.2%)	1/12	(8.3%)	0/13	(0.0%)	0/15	(0.0%)	15/20	(75.0%)
PACIFIC COAST ZONE										
Balberta	0/1	(0.0%)	0/2	(0.0%)	0/1	(0.0%)	0/2	(0.0%)	3/3	(100.0%)
Montana Complex	1/5	(20.0%)	0/6	(0.0%)	1/4	(25.0%)	0/7	(0.0%)	9/12	(75.0%)
COMBINED SAMPLE	94/202	(46.5%)	27/359	(7.5%)	16/311	(5.1%)	3/438	(0.7%)	451/547	(82.4%)

Table 6.5. Continued.

SITE	Metacone (UM2)		Metacone (UM3)		Hypocone (UM1)		Hypocone (UM2)		Hypocone (UM3)	
CENTRAL ZONE										
Tikal	107/123	(87.0%)	31/77	(43.7%)	78/135	(57.8%)	59/113	(52.2%)	39/70	(55.7%)
Tikal: Caches & Pr. Dep.	15/17	(88.2%)	11/18	(61.1%)	15/21	(71.4%)	9/17	(52.9%)	10/18	(55.6%)
Uaxactun	3/6	(50.0%)	4/5	(80.0%)	4/5	(80.0%)	2/6	(33.3%)	0/5	(0.0%)
Calakmul	17/22	(77.33%)	7/10	(70.0%)	19/27	(70.4%)	8/21	(38.1%)	5/8	(62.5%)
USUMACINTA ZONE										
Piedras Negras	36/42	(85.7%)	9/24	(37.5%)	30/51	(58.8%)	17/32	(53.1%)	11/20	(55.0%)
PASIÓN ZONE										
Altar de Sacrificios	24/26	(92.3%)	8/13	(61.5%)	26/34	(76.5%)	20/25	(80.0%)	7/10	(70.0%)
Seibal	20/23	(87.0%)	5/9	(55.6%)	13/27	(59.1%)	10/19	(52.6%)	4/8	(50.0%)
Dos Pilas	40/41	(97.6%)	8/27	(29.6%)	30/40	(75.0%)	23/37	(62.2%)	15/28	(53.6%)
Aguateca	9/9	(100.0%)	3/4	(75.0%)	7/9	(77.8%)	4/6	(66.7%)	2/4	(50.0%)
Tamarindito	8/8	(100.0%)	2/3	(66.7%)	5/8	(62.5%)	5/8	(62.5%)	1/3	(33.3%)
Itzán	5/5	(100.0%)	2/4	(50.0%)	1/3	(33.3%)	4/4	(100.0%)	1/3	(33.3%)
BELIZE ZONE										
Altun Ha	45/52	(86.5%)	9/20	(45.0%)	49/64	(76.6%)	25/39	(64.1%)	7/16	(43.8%)
Barton Ramie	14/17	(82.4%)	6/11	(54.5%)	15/18	(83.3%)	9/13	(69.2%)	6/10	(60.0%)
Baking Pot	6/6	(100.0%)	2/4	(50.0%)	8/10	(80.0%)	5/5	(100.0%)	3/4	(75.0%)
Colha	8/12	(66.7%)	3/7	(42.9%)	6/18	(33.3%)	5/10	(50.0%)	4/9	(44.4%)
SOUTHWESTERN ZONE										
Copan	28/29	(96.6%)	7/18	(38.9%)	29/33	(87.9%)	7/14	(50.0%)	4/15	(26.7%)
HIGHLANDS ZONE										
Kaminaljuyu	14/18	(77.8%)	5/6	(83.3%)	15/20	(75.0%)	10/18	(55.6%)	0/5	(0.0%)
PACIFIC COAST ZONE										
Balberta	1/2	(50.0%)	0/1	(0.0%)	3/3	(100.0%)	0/1	(0.0%)	0/1	(0.0%)
Montana Complex	6/8	(75.0%)	4/4	(100.0%)	8/12	(66.7%)	2/8	(25.0%)	1/3	(33.3%)
COMBINED SAMPLE	406/466	(87.1%)	126/259	(48.6%)	361/533	(67.7%)	224/396	(56.6%)	119/238	50.0%)

Table 6.5. Continued.

SITE	Metaconule (UM1)		Metaconule (UM2)		Metaconule (UM3)		Carabelli's (UM1)		Carabelli's (UM2)	
CENTRAL ZONE										
Tikal	13/98	(13.3%)	7/106	(6.6%)	3/70	(4.3%)	82/117	(70.1%)	15/111	(13.5%)
Tikal: Caches & Pr. Dep.	0/9	(0.0%)	1/12	(8.3%)	1/16	(6.3%)	14/17	(82.4%)	1/15	(6.7%)
Uaxactun	1/4	(25.0%)	1/5	(20.0%)	0/4	(0.0%)	3/5	(60.0%)	1/6	(16.7%)
Calakmul	3/21	(14.3%)	0/15	(0.0%)	1/8	(12.5%)	12/23	(52.2%)	1/17	(5.9%)
USUMACINTA ZONE										
Piedras Negras	6/30	(20.0%)	0/27	(0.0%)	1/22	(4.5%)	22/41	(53.7%)	0/39	(0.0%)
PASIÓN ZONE										
Altar de Sacrificios	3/14	(21.4%)	1/10	(4.3%)	1/11	(7.1%)	18/21	(85.7%)	2/23	(8.7%)
Seibal	1/11	(7.7%)	0/12	(0.0%)	0/8	(0.0%)	11/18	(61.1%)	3/18	(16.7%)
Dos Pilas	1/25	(4.0%)	0/30	(0.0%)	0/25	(0.0%)	23/32	(71.9%)	2/32	(6.3%)
Aguateca	1/7	(14.3%)	0/5	(0.0%)	0/4	(0.0%)	5/7	(71.4%)	0/8	(0.0%)
Tamarindito	0/6	(0.0%)	0/6	(0.0%)	0/3	(0.0%)	6/7	(85.7%)	0/7	(0.0%)
Itzán	0/3	(0.0%)	0/3	(0.0%)	0/2	(0.0%)	2/2	(100.0%)	1/3	(33.3%)
BELIZE ZONE										
Altun Ha	5/31	(16.1%)	1/25	(4.0%)	5/14	(35.7%)	36/53	(67.9%)	2/39	(5.1%)
Barton Ramie	1/9	(11.1%)	1/8	(12.5%)	1/8	(12.5%)	5/12	(41.7%)	1/13	(7.7%)
Baking Pot	0/2	(0.0%)	0/3	(0.0%)	0/3	(0.0%)	2/4	(50.0%)	0/5	(0.0%)
Colha	1/12	(8.3%)	0/6	(0.0%)	0/7	(0.0%)	11/13	(84.6%)	0/11	(0.0%)
SOUTHWESTERN ZONE										
Copan	1/16	(6.3%)	1/9	(11.9%)	0/14	(0.0%)	11/13	(84.6%)	0/15	(0.0%)
HIGHLANDS ZONE										
Kaminaljuyu	1/16	(6.3%)	3/18	(16.7%)	0/3	(0.0%)	11/15	(73.3%)	1/14	(0.0%)
PACIFIC COAST ZONE										
Balberta	0/1	(0.0%)	0/1	(0.0%)	0/1	(0.0%)	0/1	(0.0%)	0/1	(0.0%)
Montana Complex	2/9	(22.2%)	1/6	(16.7%)	0/2	(0.0%)	4/9	(44.4%)	0/7	(0.0%)
COMBINED SAMPLE	40/322	(12.4%)	16/315	(5.1%)	13/225	(5.8%)	277/409	(67.7%)	30/382	(7.9%)

Table 6.5. Continued.

SITE	Carabelli's (UM3)		Parastyle (UM1)		Parastyle (UM2)		Parastyle (UM3)		Enamel Ext. (UP3)	
CENTRAL ZONE										
Tikal	14/74	(18.9%)	2/127	(1.6%)	1/112	(0.9%)	2/68	(2.9%)	2/82	(2.3%)
Tikal: Caches & Pr. Dep.	0/17	(0.0%)	0/17	(0.0%)	0/16	(0.0%)	1/17	(5.9%)	0/7	(0.0%)
Uaxactun	0/5	(0.0%)	0/3	(0.0%)	1/6	(16.7%)	0/4	(0.0%)	0/4	(0.0%)
Calakmul	1/9	(11.1%)	1/19	(5.3%)	0/15	(0.0%)	1/10	(10.0%)	0/14	(0.0%)
USUMACINTA ZONE										
Piedras Negras	1/24	(4.2%)	0/46	(0.0%)	0/42	(0.0%)	0/22	(0.0%)	0/36	(0.0%)
PASIÓN ZONE										
Altar de Sacrificios	0/11	(0.0%)	1/20	(5.0%)	2/23	(8.7%)	1/12	(8.3%)	0/26	(0.0%)
Seibal	1/9	(11.1%)	0/19	(0.0%)	2/19	(10.5%)	1/9	(11.1%)	0/18	(0.0%)
Dos Pilas	0/23	(0.0%)	0/31	(0.0%)	1/33	(3.0%)	3/24	(12.5%)	0/25	(0.0%)
Aguateca	0/4	(0.0%)	0/8	(0.0%)	0/7	(0.0%)	0/4	(0.0%)	0/5	(0.0%)
Tamarindito	0/3	(0.0%)	0/6	(0.0%)	1/9	(11.1%)	0/2	(0.0%)	0/6	(0.0%)
Itzán	0/4	(0.0%)	0/2	(0.0%)	0/4	(0.0%)	0/3	(0.0%)	0/3	(0.0%)
BELIZE ZONE										
Altun Ha	0/15	(0.0%)	2/51	(3.9%)	0/42	(0.0%)	1/17	(5.9%)	0/26	(0.0%)
Barton Ramie	5/9	(55.6%)	1/11	(9.1%)	0/13	(0.0%)	0/11	(0.0%)	0/21	(0.0%)
Baking Pot	0/5	(0.0%)	0/3	(0.0%)	0/4	(0.0%)	0/4	(0.0%)	0/5	(0.0%)
Colha	1/6	(16.7%)	0/16	(0.0%)	0/12	(0.0%)	1/7	(14.3%)	0/15	(0.0%)
SOUTHWESTERN ZONE										
Copan	0/15	(0.0%)	1/21	(4.8%)	0/19	(0.0%)	2/14	(14.3%)	0/12	(0.0%)
HIGHLANDS ZONE										
Kaminaljuyu	0/4	(0.0%)	1/14	(7.1%)	1/17	(5.9%)	0/5	(0.0%)	0/5	(0.0%)
PACIFIC COAST ZONE										
Balberta	1/1	(100.0%)	0/1	(0.0%)	0/1	(0.0%)	0/1	(0.0%)	0/1	(0.0%)
Montana Complex	0/2	(0.0%)	3/10	(30.0%)	0/6	(0.0%)	0/3	(0.0%)	0/3	(0.0%)
COMBINED SAMPLE	24/240	(10.0%)	12/425	(2.8%)	9/400	(2.3%)	13/235	(5.5%)	(2/317)	(0.6%)

Table 6.5. Continued.

SITE	Enamel Ext. (UP4)		Enamel Ext. (UM1)		Enamel Ext. (UM2)		Enamel Ext. (UM3)		Root # (UP3)	
CENTRAL ZONE										
Tikal	2/77	(2.6%)	33/54	(61.1%)	29/59	49.2	26/37	(70.3%)	13/71	(18.3%)
Tikal: Caches & Pr. Dep.	0/7	(0.0%)	4/4	(100.0%)	5/6	83.3	2/3	(66.7%)	2/12	(8.7%)
Uaxactun	0/3	(0.0%)	3/3	(100.0%)	1/1	100.0	1/1	(100.0%)	0/3	(0.0%)
Calakmul	0/11	(0.0%)	3/7	(42.9%)	3/5	60.0	1/3	(33.3%)	1/16	(6.3%)
USUMACINTA ZONE										
Piedras Negras	1/37	(2.7%)	16/22	(72.7%)	19/31	61.3	11/15	(73.3%)	9/37	(24.3%)
PASIÓN ZONE										
Altar de Sacrificios	0/22	(0.0%)	11/16	(68.8%)	9/15	60.0	5/6	(83.3%)	4/16	(25.0%)
Seibal	0/21	(0.0%)	12/17	(70.6%)	8/17	47.1	2/4	(50.0%)	3/19	(15.8%)
Dos Pilas	2/29	(6.9%)	18/23	(78.3%)	12/28	42.9	13/19	(68.4%)	2/32	(6.3%)
Aguateca	0/9	(0.0%)	4/4	(100.0%)	3/4	75.0	3/3	(100.0%)	0/9	(0.0%)
Tamarindito	0/5	(0.0%)	3/3	(100.0%)	3/6	50.0	3/3	(100.0%)	0/3	(0.0%)
Itzán	0/4	(0.0%)	-----	-----	0/1	0.0	-----	-----	0/2	(0.0%)
BELIZE ZONE										
Altun Ha	0/24	(0.0%)	17/19	(89.5%)	14/21	66.7	6/7	(85.7%)	8/26	(30.8%)
Barton Ramie	0/15	(0.0%)	4/8	(50.0%)	10/12	83.3	5/8	(62.5%)	6/18	(33.3%)
Baking Pot	0/3	(0.0%)	2/3	(66.7%)	2/3	66.7	2/3	(66.7%)	1/3	(33.3%)
Colha	0/13	(0.0%)	0/5	(0.0%)	3/7	42.9	3/8	(37.5%)	5/12	(41.7%)
SOUTHWESTERN ZONE										
Copan	0/14	(0.0%)	5/11	(45.5%)	9/14	64.3	2/6	(33.3%)	4/19	(21.1%)
HIGHLANDS ZONE										
Kaminaljuyu	0/5	(0.0%)	1/1	(100.0%)	4/4	100.0	1/1	(100.0%)	0/1	(0.0%)
PACIFIC COAST ZONE										
Balberta	0/1	(0.0%)	1/1	(100.0%)	0/1	0.0	0/1	(0.0%)	0/1	(0.0%)
Montana Complex	1/5	(20.0%)	5/8	(62.5%)	1/3	33.3	-----	-----	0/1	(0.0%)
COMBINED SAMPLE	6/303	(2.0%)	142/209	(67.9%)	135/238	(56.7%)	90/128	(70.3%)	58/303	(19.1%)

Table 6.5. Continued.

SITE	Root # (UP4)		Root # (UM1)		Root # (UM2)		Root # (UM3)		Peg Incisor (UI2)	
CENTRAL ZONE										
Tikal	0/65	(0.0%)	5/77	(6.5%)	28/66	(42.4%)	8/46	(17.4%)	7/84	(8.3%)
Tikal: Caches & Pr. Dep.	0/10	(0.0%)	0/11	(0.0%)	6/8	(75.0%)	2/9	(22.2%)	5/19	(26.3%)
Uaxactun	0/2	(0.0%)	0/1	(0.0%)	-----	-----	0/1	(0.0%)	1/4	(25.0%)
Calakmul	0/12	(0.0%)	1/19	(5.3%)	4/6	(66.7%)	1/6	(16.7%)	2/18	(11.1%)
USUMACINTA ZONE										
Piedras Negras	0/36	(0.0%)	1/43	(2.3%)	8/30	(26.7%)	0/19	(0.0%)	4/42	(9.5%)
PASIÓN ZONE										
Altar de Sacrificios	0/13	(0.0%)	0/22	(0.0%)	10/15	(66.7%)	4/11	(36.4%)	0/28	(2.8%)
Seibal	0/15	(0.0%)	0/20	(0.0%)	12/19	(63.2%)	1/3	(33.3%)	4/14	(28.6%)
Dos Pilas	0/32	(0.0%)	2/34	(5.9%)	18/32	(56.3%)	5/23	(21.7%)	1/34	(2.9%)
Aguateca	0/9	(0.0%)	0/4	(0.0%)	2/4	(50.0%)	1/3	(33.3%)	2/9	(22.2%)
Tamarindito	0/3	(0.0%)	0/6	(0.0%)	1/1	(100.0%)	3/3	(100.0%)	0/9	(0.0%)
Itzán	0/3	(0.0%)	0/2	(0.0%)	0/2	(0.0%)	1/3	(33.3%)	0/4	(0.0%)
BELIZE ZONE										
Altun Ha	0/27	(0.0%)	0/36	(2.1%)	15/29	(51.7%)	5/20	(25.0%)	7/45	(15.6%)
Barton Ramie	3/17	(14.3%)	0/14	(0.0%)	8/15	(53.3%)	4/9	(44.4%)	3/20	(15.0%)
Baking Pot	0/3	(0.0%)	0/4	(0.0%)	1/1	(100.0%)	1/2	(50.0%)	0/7	(0.0%)
Colha	0/9	(0.0%)	0/9	(0.0%)	5/9	(55.6%)	2/7	(28.6%)	0/15	(0.0%)
SOUTHWESTERN ZONE										
Copan	0/18	(0.0%)	2/17	(11.8%)	7/15	(46.7%)	1/12	(8.3%)	2/20	(10.0%)
HIGHLANDS ZONE										
Kaminaljuyu	0/1	(0.0%)	0/5	(0.0%)	2/4	(50.0%)	0/1	(0.0%)	0/9	(0.0%)
PACIFIC COAST ZONE										
Balberta	0/1	(0.0%)	1/3	(33.3%)	1/1	(100.0%)	0/1	(0.0%)	0/2	(0.0%)
Montana Complex	0/2	(0.0%)	0/2	(0.0%)	1/1	(100.0%)	0/1	(0.0%)	2/7	(28.6%)
COMBINED SAMPLE	3/278	(1.1%)	12/329	(3.6%)	129/258	(50.0%)	39/180	(21.7%)	40/390	(10.3%)

Table 6.5. Continued.

SITE	Peg Molar (UM3)		Odontome (UP3)		Odontome (UP4)		Con. Absence (UI2)		Con. Absence (UP3)	
CENTRAL ZONE										
Tikal	10/75	(13.3%)	1/127	(0.8%)	1/115	(0.9%)	0/105	(0.0%)	1/128	(0.7%)
Tikal: Caches & Pr. Dep.	1/17	(5.9%)	0/22	(0.0%)	2/21	(9.5%)	0/22	(0.0%)	0/23	(0.0%)
Uaxactun	0/5	(0.0%)	0/7	(0.0%)	0/7	(0.0%)	0/4	(0.0%)	0/7	(0.0%)
Calakmul	0/13	(0.0%)	0/27	(0.0%)	0/21	(0.0%)	0/17	(0.0%)	0/25	(0.0%)
USUMACINTA ZONE										
Piedras Negras	2/26	(7.7%)	0/40	(0.0%)	1/42	(2.4%)	0/50	(0.0%)	1/53	(1.9%)
PASIÓN ZONE										
Altar de Sacrificios	2/19	(10.5%)	0/27	(0.0%)	0/24	(0.0%)	0/32	(0.0%)	0/34	(0.0%)
Seibal	1/10	(0.0%)	0/22	(0.0%)	0/23	(0.0%)	0/18	(0.0%)	0/25	(0.0%)
Dos Pilas	3/30	(10.0%)	0/42	(0.0%)	0/40	(0.0%)	0/33	(0.0%)	0/41	(0.0%)
Aguateca	1/5	(20.0%)	0/11	(0.0%)	0/9	(0.0%)	0/10	(0.0%)	0/10	(0.0%)
Tamarindito	0/4	(0.0%)	0/10	(0.0%)	0/8	(0.0%)	0/9	(0.0%)	0/8	(0.0%)
Itzán	0/4	(0.0%)	0/4	(0.0%)	0/4	(0.0%)	0/5	(0.0%)	0/5	(0.0%)
BELIZE ZONE										
Altun Ha	7/30	(23.3%)	1/50	(2.0%)	0/46	(0.0%)	0/49	(0.0%)	0/56	(0.0%)
Barton Ramie	1/13	(7.7%)	0/22	(0.0%)	0/19	(0.0%)	0/22	(0.0%)	0/24	(0.0%)
Baking Pot	0/5	(0.0%)	0/7	(0.0%)	0/5	(0.0%)	0/9	(0.0%)	0/9	(0.0%)
Colha	2/10	(20.0%)	0/18	(0.0%)	0/11	(0.0%)	0/16	(0.0%)	0/16	(0.0%)
SOUTHWESTERN ZONE										
Copan	3/24	(12.5%)	0/25	(0.0%)	0/22	(0.0%)	0/20	(0.0%)	0/30	(0.0%)
HIGHLANDS ZONE										
Kaminaljuyu	1/5	(20.0%)	1/16	(6.3%)	1/17	(5.9%)	0/12	(0.0%)	0/20	(0.0%)
PACIFIC COAST ZONE										
Balberta	1/1	(100.0%)	0/2	(0.0%)	0/3	(0.0%)	0/2	(0.0%)	0/3	(0.0%)
Montana Complex	0/4	(0.0%)	0/9	(0.0%)	0/6	(0.0%)	0/10	(0.0%)	0/8	(0.0%)
COMBINED SAMPLE	35/300	(11.7%)	3/487	(0.6%)	6/445	(1.3%)	0/444	(0.0%)	2/525	(0.4%)

Table 6.5. Continued.

SITE	Con. Absence (UM3)	Shoveling (LI1)	Dis. Acc. Ridge (LC)	Lingual Csp # (LP3)	Lingual Csp # (LP4)
CENTRAL ZONE					
Tikal	2/88 (2.1%)	48/92 (52.2%)	59/67 (88.1%)	24/93 (25.8%)	40/90 (44.4%)
Tikal: Caches & Pr. Dep.	1/22 (4.3%)	6/12 (50.0%)	1/6 (16.7%)	3/5 (60.0%)	11/15 (73.3%)
Uaxactun	0/6 (0.0%)	3/3 (100.0%)	2/2 (100.0%)	3/5 (60.0%)	4/4 (100.0%)
Calakmul	0/14 (0.0%)	14/25 (56.0%)	9/10 (90.0%)	6/20 (30.0%)	9/28 (32.1%)
USUMACINTA ZONE					
Piedras Negras	1/28 (3.6%)	17/41 (41.5%)	13/22 (59.1%)	5/35 (14.3%)	7/19 (20.0%)
PASIÓN ZONE					
Altar de Sacrificios	3/23 (13.0%)	6/15 (40.0%)	6/10 (60.0%)	9/12 (75.0%)	7/19 (36.8%)
Seibal	1/13 (7.7%)	3/8 (37.5%)	2/3 (66.6%)	6/8 (75.0%)	6/9 (66.7%)
Dos Pilas	0/30 (0.0%)	11/32 (34.4%)	12/16 (75.0%)	12/31 (38.7%)	15/32 (46.9%)
Aguateca	0/6 (0.0%)	3/7 (42.9%)	1/6 (16.7%)	4/10 (40.0%)	6/9 (66.7%)
Tamarindito	0/4 (0.0%)	1/4 (25.0%)	2/2 (100.0%)	3/6 (50.0%)	1/8 (12.5%)
Itzán	0/4 (0.0%)	2/3 (66.7%)	1/2 (50.0%)	1/3 (33.3%)	1/4 (25.0%)
BELIZE ZONE					
Altun Ha	0/30 (0.0%)	15/36 (41.7%)	9/19 (47.4%)	15/23 (65.2%)	18/29 (62.1%)
Barton Ramie	0/12 (0.0%)	6/14 (42.9%)	1/6 (16.7%)	9/12 (75.0%)	3/11 (27.3%)
Baking Pot	1/7 (14.3%)	1/3 (33.3%)	0/2 (0.0%)	0/1 (0.0%)	1/2 (50.0%)
Colha	1/12 (8.3%)	12/15 (80.0%)	3/3 (100.0%)	1/12 (8.3%)	3/8 (37.5%)
SOUTHWESTERN ZONE					
Copan	2/27 (7.4%)	2/8 (25.0%)	4/6 (66.7%)	5/9 (55.6%)	7/17 (41.2%)
HIGHLANDS ZONE					
Kaminaljuyu	0/9 (0.0%)	6/11 (54.5%)	8/11 (72.7%)	4/12 (33.3%)	7/12 (58.3%)
PACIFIC COAST ZONE					
Balberta	0/2 (0.0%)	0/2 (0.0%)	1/2 (50.0%)	1/1 (100.0%)	0/2 (0.0%)
Montana Complex	0/5 (0.0%)	1/6 (16.7%)	2/3 (66.7%)	6/6 (100.0%)	2/4 (50.0%)
COMBINED SAMPLE	12/342 (3.5%)	155/333 (46.5%)	136/198 (68.7%)	117/304 (38.5%)	148/338 (43.8%)

Table 6.5. Continued.

SITE	Ant. Fovea (LM1)		Ant. Fovea (LM2)		Ant. Fovea (LM3)		Groove (LM1)		Groove (LM2)	
CENTRAL ZONE										
Tikal	46/124	(37.1%)	66/86	(76.7%)	27/64	(42.2%)	45/153	(29.4%)	78/119	(65.5%)
Tikal: Caches & Pr. Dep.	3/20	(15.0%)	13/14	(92.9%)	9/15	(60.0%)	4/23	(17.4%)	13/20	(65.0%)
Uaxactun	1/7	(14.3%)	4/5	(80.0%)	4/4	(100.0%)	2/7	(28.6%)	2/7	(28.6%)
Calakmul	0/15	(0.0%)	8/19	(42.1%)	5/9	(55.6%)	5/25	(20.0%)	19/30	(63.3%)
USUMACINTA ZONE										
Piedras Negras	10/33	(31.3%)	20/29	(69.0%)	9/19	(47.4%)	8/52	(15.4%)	29/48	(60.4%)
PASIÓN ZONE										
Altar de Sacrificios	0/18	(0.0%)	11/17	(64.7%)	7/13	(53.8%)	9/34	(26.5%)	18/27	(66.7%)
Seibal	0/11	(0.0%)	4/7	(57.1%)	2/4	(50.0%)	3/25	(12.0%)	13/18	(72.2%)
Dos Pilas	11/27	(40.7%)	14/21	(66.7%)	6/22	(27.3%)	6/37	(16.2%)	25/39	(64.1%)
Aguateca	3/4	(75.0%)	1/2	(50.0%)	2/5	(40.0%)	3/7	(42.9%)	3/5	(60.0%)
Tamarindito	0/5	(0.0%)	2/5	(40.0%)	2/5	(40.0%)	3/6	(50.0%)	4/5	(80.0%)
Itzán	0/4	(0.0%)	2/4	(50.0%)	2/3	(66.7%)	3/5	(60.0%)	3/4	(75.0%)
BELIZE ZONE										
Altun Ha	4/41	(9.8%)	19/30	(63.3%)	4/12	(33.3%)	14/68	(20.6%)	30/49	(61.2%)
Barton Ramie	0/10	(0.0%)	7/10	(70.0%)	2/4	(50.0%)	6/22	(27.3%)	14/20	(70.0%)
Baking Pot	0/2	(0.0%)	-----	-----	3/9	(33.3%)	2/4	(50.0%)	2/5	(40.0%)
Colha	7/11	(63.6%)	3/7	(42.9%)	2/5	(40.0%)	1/17	(5.9%)	6/11	(54.5%)
SOUTHWESTERN ZONE										
Copan	1/15	(6.7%)	7/11	(63.6%)	3/9	(33.3%)	5/13	(13.3%)	12/23	(52.2%)
HIGHLANDS ZONE										
Kaminaljuyu	2/8	(25.0%)	11/14	(78.6%)	2/4	(50.0%)	5/14	(38.5%)	9/19	(47.4%)
PACIFIC COAST ZONE										
Balberta	0/2	(0.0%)	1/1	(100.0%)	0/1	(0.0%)	1/3	(33.3%)	1/3	(33.3%)
Montana Complex	3/5	(60.0%)	5/6	(83.3%)	1/1	(100.0%)	5/10	(50.0%)	5/10	(50.0%)
COMBINED SAMPLE	91/361	(25.2%)	198/288	(68.8%)	87/198	(43.9%)	129/541	(23.8%)	286/462	(61.9%)

Table 6.5. Continued.

SITE	Groove (LM3)		Cusp # (LM1)		Cusp # (LM2)		Cusp # (LM3)		Def. Wrinkle (LM1)	
CENTRAL ZONE										
Tikal	77/86	(89.5%)	60/125	(48.0%)	58/78	(74.4%)	29/77	(37.7%)	41/133	(30.8%)
Tikal: Caches & Pr. Dep.	16/18	(88.9%)	11/21	(52.4%)	13/14	(92.9%)	13/17	(76.5%)	5/24	(20.8%)
Uaxactun	3/5	(60.0%)	3/7	(42.9%)	2/3	(66.7%)	3/5	(60.0%)	0/7	(0.0%)
Calakmul	12/16	(75.0%)	7/14	(50.0%)	14/21	(66.7%)	1/12	(8.3%)	7/25	(28.0%)
USUMACINTA ZONE										
Piedras Negras	22/27	(81.5%)	19/38	(50.0%)	17/31	(54.8%)	6/25	(24.0%)	18/37	(48.6%)
PASIÓN ZONE										
Altar de Sacrificios	19/21	(90.5%)	11/19	(57.9%)	7/12	(58.3%)	6/15	(40.0%)	7/26	(26.9%)
Seibal	7/10	(70.0%)	5/15	(33.3%)	6/7	(85.7%)	6/8	(75.0%)	5/18	(27.8%)
Dos Pilas	28/29	(96.6%)	16/24	(66.7%)	11/16	(68.8%)	7/22	(31.8%)	2/28	(7.1%)
Aguateca	6/8	(75.0%)	1/3	(33.3%)	3/3	(100.0%)	5/7	(71.4%)	0/5	(0.0%)
Tamarindito	5/6	(83.3%)	2/5	(40.0%)	1/2	(50.0%)	4/5	(80.0%)	0/5	(0.0%)
Itzán	3/4	(75.0%)	1/4	(25.0%)	1/3	(33.3%)	1/4	(25.0%)	1/4	(25.0%)
BELIZE ZONE										
Altun Ha	22/27	(81.5%)	19/42	(45.2%)	17/23	(73.9%)	7/15	(46.7%)	18/52	(34.6%)
Barton Ramie	6/6	(100.0%)	8/14	(57.1%)	7/10	(70.0%)	1/5	(20.0%)	3/14	(21.4%)
Baking Pot	2/2	(100.0%)	1/3	(33.3%)	1/1	(100.0%)	1/1	(100.0%)	0/2	(0.0%)
Colha	9/9	(100.0%)	7/11	(63.6%)	4/4	(100.0%)	2/7	(28.6%)	0/15	(0.0%)
SOUTHWESTERN ZONE										
Copan	15/16	(93.8%)	5/13	(38.5%)	9/11	(81.8%)	2/9	(22.2%)	3/15	(20.0%)
HIGHLANDS ZONE										
Kaminaljuyu	9/10	(90.0%)	8/11	(72.7%)	9/10	(90.0%)	2/4	(50.0%)	2/10	(20.0%)
PACIFIC COAST ZONE										
Balberta	1/1	(100.0%)	2/2	(100.0%)	1/1	(100.0%)	1/1	(100.0%)	0/3	(0.0%)
Montana Complex	0/2	(0.0%)	4/6	(66.7%)	5/7	(71.4%)	0/2	(0.0%)	3/7	(42.9%)
COMBINED SAMPLE	262/303	(86.5%)	190/376	(50.5%)	186/257	(72.4%)	97/241	(40.2%)	115/429	(26.8%)

Table 6.5. Continued.

SITE	Def. Wrinkle (LM2)	Def. Wrinkle (LM3)	Dist. Trigonid (LM1)	Dist. Trigonid (LM2)	Dist. Trigonid (LM3)
CENTRAL ZONE					
Tikal	4/109 (3.7%)	4/75 (5.3%)	12/129 (9.3%)	2/107 (1.9%)	4/74 (5.4%)
Tikal: Caches & Pr. Dep.	0/16 (0.0%)	0/18 (0.0%)	1/21 (4.8%)	0/16 (0.0%)	1/18 (5.6%)
Uaxactun	0/6 (0.0%)	0/5 (0.0%)	0/7 (0.0%)	0/5 (0.0%)	0/4 (0.0%)
Calakmul	2/26 (7.7%)	0/15 (0.0%)	0/20 (0.0%)	0/26 (0.0%)	0/14 (0.0%)
USUMACINTA ZONE					
Piedras Negras	1/37 (2.7%)	1/20 (5.0%)	0/40 (0.0%)	0/38 (0.0%)	0/23 (0.0%)
PASIÓN ZONE					
Altar de Sacrificios	0/14 (0.0%)	0/13 (0.0%)	1/20 (5.0%)	0/17 (0.0%)	0/13 (0.0%)
Seibal	0/12 (0.0%)	1/5 (20.0%)	0/16 (0.0%)	0/13 (0.0%)	0/6 (0.0%)
Dos Pilas	0/25 (0.0%)	1/23 (4.3%)	0/28 (0.0%)	0/27 (0.0%)	2/23 (8.7%)
Aguateca	0/2 (0.0%)	1/6 (0.0%)	0/6 (0.0%)	0/2 (0.0%)	0/6 (0.0%)
Tamarindito	0/4 (0.0%)	0/6 (0.0%)	1/5 (20.0%)	0/4 (0.0%)	0/6 (0.0%)
Itzán	0/4 (0.0%)	0/4 (0.0%)	1/4 (25.0%)	0/4 (0.0%)	0/4 (0.0%)
BELIZE ZONE					
Altun Ha	2/37 (5.4%)	0/14 (0.0%)	1/43 (2.3%)	0/34 (0.0%)	0/13 (0.0%)
Barton Ramie	0/14 (0.0%)	0/5 (0.0%)	0/14 (0.0%)	0/13 (0.0%)	0/5 (0.0%)
Baking Pot	0/1 (0.0%)	0/1 (0.0%)	0/2 (0.0%)	0/3 (0.0%)	0/1 (0.0%)
Colha	1/6 (0.0%)	0/7 (0.0%)	0/14 (0.0%)	0/6 (0.0%)	0/5 (0.0%)
SOUTHWESTERN ZONE					
Copan	1/12 (0.0%)	0/8 (0.0%)	0/14 (0.0%)	0/14 (0.0%)	0/9 (0.0%)
HIGHLANDS ZONE					
Kaminaljuyu	0/12 (0.0%)	0/6 (0.0%)	0/10 (0.0%)	0/16 (0.0%)	0/7 (0.0%)
PACIFIC COAST ZONE					
Balberta	0/1 (0.0%)	0/1 (0.0%)	0/3 (0.0%)	0/1 (0.0%)	1/1 (100.0%)
Montana Complex	0/9 (0.0%)	0/1 (0.0%)	1/8 (12.5%)	0/8 (0.0%)	0/2 (0.0%)
COMBINED SAMPLE	11/347 (3.2%)	8/233 (3.4%)	18/402 (4.5%)	2/350 (0.6%)	8/234 (3.4%)

Table 6.5. Continued.

SITE	Protostylid (LM1)		Protostylid (LM2)		Protostylid (LM3)		Hypoconulid (LM1)		Hypoconulid (LM2)	
CENTRAL ZONE										
Tikal	49/130	(37.7%)	45/101	(44.6%)	39/69	(56.5%)	44/130	(33.8%)	54/80	(67.5%)
Tikal: Caches & Pr. Dep.	6/20	(30.0%)	7/16	(43.8%)	9/15	(60.0%)	7/20	(35.0%)	12/14	(85.7%)
Uaxactun	3/6	(50.0%)	4/4	(100.0%)	3/4	(75.0%)	2/7	(28.6%)	2/3	(66.7%)
Calakmul	10/21	(47.6%)	9/21	(42.9%)	11/12	(91.7%)	2/13	(15.4%)	14/21	(66.7%)
USUMACINTA ZONE										
Piedras Negras	12/49	(24.5%)	14/37	(37.8%)	11/25	(44.0%)	13/38	(34.2%)	15/30	(50.0%)
PASIÓN ZONE										
Altar de Sacrificios	9/17	(52.9%)	1/9	(11.1%)	8/12	(66.7%)	7/19	(36.8%)	7/12	(58.3%)
Seibal	3/12	(25.0%)	3/8	(37.5%)	6/7	(85.7%)	11/16	(68.8%)	6/7	(85.7%)
Dos Pilas	17/14	(45.2%)	18/29	(62.1%)	11/23	(47.8%)	2/26	(7.7%)	11/16	(68.8%)
Aguateca	4/8	(50.0%)	1/5	(20.0%)	2/5	(40.0%)	2/3	(66.7%)	3/3	(100.0%)
Tamarindito	3/6	(50.0%)	2/4	(50.0%)	1/4	(25.0%)	3/5	(60.0%)	1/2	(50.0%)
Itzán	2/4	(50.0%)	1/4	(25.0%)	0/4	(0.0%)	2/4	(50.0%)	1/3	(33.3%)
BELIZE ZONE										
Altun Ha	16/40	(40.0%)	15/26	(57.7%)	8/15	(53.3%)	16/42	(38.1%)	16/23	(69.6%)
Barton Ramie	5/9	(55.6%)	6/8	(75.0%)	4/5	(80.0%)	4/14	(28.6%)	7/9	(77.8%)
Baking Pot	1/2	(50.0%)	1/2	(50.0%)	1/1	(100.0%)	0/3	(0.0%)	2/2	(100.0%)
Colha	5/15	(33.3%)	1/8	(12.5%)	4/8	(50.0%)	5/13	(38.5%)	4/4	(100.0%)
SOUTHWESTERN ZONE										
Copan	9/17	(52.9%)	10/12	(83.3%)	6/8	(66.6%)	4/13	(30.8%)	7/9	(77.8%)
HIGHLANDS ZONE										
Kaminaljuyu	6/8	(75.0%)	12/14	(85.7%)	2/3	(80.0%)	2/11	(18.2%)	9/10	(90.0%)
PACIFIC COAST ZONE										
Balberta	1/3	(33.3%)	1/1	(100.0%)	0/1	(0.0%)	0/2	(0.0%)	1/1	(100.0%)
Montana Complex	4/8	(50.0%)	5/5	(100.0%)	2/2	(100.0%)	2/6	(33.3%)	3/4	(75.0%)
COMBINED SAMPLE	162/406	(39.9%)	156/314	(49.7%)	128/223	(57.4%)	128/384	(33.3%)	175/253	(69.2%)

Table 6.5. Continued.

SITE	Hypoconulid (LM3)		Entoconulid (LM1)		Entoconulid (LM2)		Entoconulid (LM3)		Metaconulid (LM1)	
CENTRAL ZONE										
Tikal	56/74	(75.7%)	60/123	(48.8%)	22/80	(27.5%)	28/72	(36.7%)	9/141	(6.4%)
Tikal: Caches & Pr. Dep.	16/16	(100.0%)	10/20	(50.0%)	7/14	(50.0%)	13/17	(77.8%)	2/25	(8.0%)
Uaxactun	5/5	(100.0%)	3/7	(42.9%)	1/3	(33.3%)	3/4	(75.0%)	1/8	(12.5%)
Calakmul	5/12	(41.7%)	6/13	(46.2%)	5/21	(23.8%)	1/12	(8.3%)	2/26	(7.7%)
USUMACINTA ZONE										
Piedras Negras	17/24	(70.8%)	17/36	(47.2%)	3/30	(10.0%)	6/22	(27.3%)	4/50	(8.0%)
PASIÓN ZONE										
Altar de Sacrificios	10/14	(71.4%)	11/19	(5.9%)	4/12	(33.3%)	5/15	(33.3%)	2/26	(7.7%)
Seibal	8/8	(100.0%)	5/15	(33.3%)	5/7	(71.4%)	5/7	(62.5%)	7/22	(31.8%)
Dos Pilas	14/22	(63.6%)	14/22	(63.6%)	3/15	(20.0%)	7/22	(31.8%)	2/37	(5.4%)
Aguateca	7/7	(100.0%)	1/3	(33.3%)	1/3	(33.3%)	5/7	(71.4%)	1/8	(12.5%)
Tamarindito	4/5	(80.0%)	2/5	(40.0%)	0/2	(0.0%)	4/5	(80.0%)	2/6	(33.3%)
Itzán	2/4	(50.0%)	1/4	(25.0%)	0/3	(0.0%)	1/4	(25.0%)	0/4	(0.0%)
BELIZE ZONE										
Altun Ha	11/14	(78.6%)	18/40	(45.0%)	4/24	(16.7%)	6/14	(33.3%)	3/57	(5.3%)
Barton Ramie	4/5	(80.0%)	7/13	(53.8%)	2/12	(20.0%)	1/5	(16.7%)	0/18	(0.0%)
Baking Pot	1/1	(100.0%)	1/3	(33.3%)	1/1	(100.0%)	1/1	(100.0%)	0/3	(0.0%)
Colha	3/4	(75.0%)	7/11	(63.6%)	1/5	(20.0%)	2/4	(50.0%)	0/16	(0.0%)
SOUTHWESTERN ZONE										
Copan	6/9	(66.7%)	5/13	(38.5%)	1/9	(11.1%)	2/9	(22.2%)	2/28	(7.1%)
HIGHLANDS ZONE										
Kaminaljuyu	3/4	(75.0%)	8/11	(72.7%)	4/10	(40.0%)	2/4	(50.0%)	0/11	(0.0%)
PACIFIC COAST ZONE										
Balberta	1/1	(100.0%)	2/2	(100.0%)	-----	-----	1/1	(100.0%)	0/3	(0.0%)
Montana Complex	1/2	(50.0%)	4/6	(66.7%)	1/4	(25.0%)	0/2	(0.0%)	3/9	(33.3%)
COMBINED SAMPLE	174/231	(75.3%)	182/365	(49.9%)	65/253	(25.7%)	93/227	(41.0%)	40/495	(8.1%)

Table 6.5. Continued.

SITE	Metaconulid (LM2)	Metaconulid (LM3)	Enamel Ext. (LP3)	Enamel Ext. (LP4)	Enamel Ext. (LM1)
CENTRAL ZONE					
Tikal	2/116 (1.7%)	3/78 (3.8%)	0/80 (0.0%)	1/78 (1.3%)	5/57 (8.8%)
Tikal: Caches & Pr. Dep.	0/20 (0.0%)	0/18 (0.0%)	0/5 (0.0%)	0/10 (0.0%)	2/12 (6.7%)
Uaxactun	0/6 (0.0%)	0/4 (0.0%)	0/2 (0.0%)	1/1 (100.0%)	1/4 (25.0%)
Calakmul	0/29 (0.0%)	0/15 (0.0%)	0/16 (0.0%)	0/9 (0.0%)	3/6 (50.0%)
USUMACINTA ZONE					
Piedras Negras	1/48 (2.1%)	0/25 (0.0%)	0/44 (0.0%)	2/45 (4.4%)	5/31 (16.1%)
PASIÓN ZONE					
Altar de Sacrificios	0/22 (0.0%)	0/15 (0.0%)	0/22 (0.0%)	0/23 (0.0%)	4/20 (20.0%)
Seibal	0/16 (0.0%)	0/5 (0.0%)	0/17 (0.0%)	0/20 (0.0%)	2/13 (15.4%)
Dos Pilas	0/31 (0.0%)	0/24 (0.0%)	0/27 (0.0%)	0/30 (0.0%)	7/20 (35.0%)
Aguateca	0/6 (0.0%)	0/8 (0.0%)	0/7 (0.0%)	0/10 (0.0%)	0/5 (0.0%)
Tamarindito	0/5 (0.0%)	0/6 (0.0%)	0/4 (0.0%)	0/6 (0.0%)	1/3 (33.3%)
Itzán	0/4 (0.0%)	0/4 (0.0%)	0/2 (0.0%)	0/2 (0.0%)	0/1 (0.0%)
BELIZE ZONE					
Altun Ha	2/39 (5.1%)	0/18 (0.0%)	0/22 (0.0%)	0/24 (0.0%)	6/22 (27.3%)
Barton Ramie	0/15 (0.0%)	0/6 (0.0%)	0/18 (0.0%)	0/24 (0.0%)	3/9 (33.3%)
Baking Pot	0/2 (0.0%)	0/1 (0.0%)	0/2 (0.0%)	0/2 (0.0%)	0/1 (0.0%)
Colha	0/12 (0.0%)	1/7 (14.3%)	0/10 (0.0%)	0/10 (0.0%)	0/8 (0.0%)
SOUTHWESTERN ZONE					
Copan	1/21 (4.8%)	0/9 (0.0%)	1/15 (6.7%)	1/15 (6.7%)	5/14 (35.7%)
HIGHLANDS ZONE					
Kaminaljuyu	0/16 (0.0%)	0/7 (0.0%)	0/2 (0.0%)	0/3 (0.0%)	1/4 (25.0%)
PACIFIC COAST ZONE					
Balberta	0/1 (0.0%)	0/1 (0.0%)	0/2 (0.0%)	0/2 (0.0%)	1/3 (33.3%)
Montana Complex	0/8 (0.0%)	0/2 (0.0%)	0/4 (0.0%)	0/3 (0.0%)	1/5 (20.0%)
COMBINED SAMPLE	6/417 (1.4%)	4/253 (1.6%)	1/306 (0.3%)	5/312 (1.6%)	47/238 (19.7%)

Table 6.5. Continued.

SITE	Enamel Ext. (LM2)	Enamel Ext. (LM3)	Tomes' Root (LP3)	Root # (LP3)	Root # (LP4)
CENTRAL ZONE					
Tikal	39/68 (57.4%)	18/45 (40.0%)	27/71 38.0	2/86 (2.3%)	0/65 (0.0%)
Tikal: Caches & Pr. Dep.	4/9 (44.4%)	4/6 (66.7%)	3/3 100.0	0/7 (0.0%)	0/8 (0.0%)
Uaxactun	2/4 (50.0%)	5/5 (100.0%)	----- -----	0/3 (0.0%)	0/3 (0.0%)
Calakmul	7/8 (87.5%)	3/5 (60.0%)	1/10 10.0	0/17 (0.0%)	0/14 (0.0%)
USUMACINTA ZONE					
Piedras Negras	25/37 (67.6%)	4/14 (28.6%)	14/38 36.8	3/46 (6.5%)	0/42 (0.0%)
PASIÓN ZONE					
Altar de Sacrificios	13/16 (81.3%)	5/9 (60.0%)	6/11 54.5	0/23 (0.0%)	0/21 (0.0%)
Seibal	8/12 (66.7%)	1/5 (20.0%)	8/16 50.0	0/19 (0.0%)	0/19 (0.0%)
Dos Pilas	13/26 (50.0%)	7/18 (38.9%)	7/23 30.4	0/27 (0.0%)	0/31 (0.0%)
Aguateca	2/6 (33.3%)	2/4 (50.0%)	0/6 0.0	0/10 (0.0%)	0/11 (0.0%)
Tamarindito	3/3 (100.0%)	1/2 (50.0%)	0/3 0.0	0/3 (0.0%)	0/3 (0.0%)
Itzán	0/1 (0.0%)	0/1 (0.0%)	1/2 50.0	0/3 (0.0%)	0/3 (0.0%)
BELIZE ZONE					
Altun Ha	14/26 (53.8%)	7/14 (50.0%)	3/7 42.9	0/25 (0.0%)	0/30 (0.0%)
Barton Ramie	9/11 (81.8%)	7/8 (87.5%)	4/18 22.2	0/21 (0.0%)	0/19 (0.0%)
Baking Pot	1/1 (100.0%)	0/1 (0.0%)	3/4 75.0	----- -----	----- -----
Colha	2/5 (40.0%)	0/3 (0.0%)	3/4 75.0	0/8 (0.0%)	0/8 (0.0%)
SOUTHWESTERN ZONE					
Copan	12/17 (70.6%)	6/11 (54.5%)	5/13 38.5	0/19 (0.0%)	0/16 (0.0%)
HIGHLANDS ZONE					
Kaminaljuyu	2/4 (50.0%)	1/2 (50.0%)	1/2 50.0	0/2 (0.0%)	0/1 (0.0%)
PACIFIC COAST ZONE					
Balberta	1/1 (100.0%)	1/1 (100.0%)	----- -----	----- -----	----- -----
Montana Complex	3/6 (50.0%)	2/2 (100.0%)	1/1 100.0	0/2 (0.0%)	0/2 (0.0%)
COMBINED SAMPLE	160/261 (61.3%)	74/156 (47.4%)	84/228 (36.8%)	5/321 (1.6%)	0/283 (0.0%)

Table 6.5. Continued.

SITE	Root # (LM1)		Root # (LM2)		Root # (LM3)		Odontome (LP3)		Odontome (LP4)	
CENTRAL ZONE										
Tikal	3/65	(4.6%)	56/68	(82.4%)	32/45	(71.1%)	3/116	(2.6%)	4/102	(3.9%)
Tikal: Caches & Pr. Dep.	1/15	(6.7%)	10/13	(76.9%)	6/11	(54.5%)	1/10	(10.0%)	2/18	(11.1%)
Uaxactun	0/5	(0.0%)	1/2	(50.0%)	2/3	(66.7%)	1/5	(20.0%)	0/6	(0.0%)
Calakmul	1/12	(8.3%)	10/13	(76.9%)	7/9	(77.8%)	1/28	(3.6%)	1/28	(3.6%)
USUMACINTA ZONE										
Piedras Negras	3/38	(7.9%)	29/35	(82.9%)	12/21	(57.1%)	0/40	(0.0%)	1/39	(2.6%)
PASIÓN ZONE										
Altar de Sacrificios	1/17	(5.9%)	12/15	(80.0%)	9/11	(81.8%)	0/27	(0.0%)	0/23	(0.0%)
Seibal	1/18	(5.6%)	13/15	(86.7%)	3/5	(60.0%)	1/10	(4.5%)	0/23	(0.0%)
Dos Pilas	0/25	(0.0%)	23/32	(71.9%)	14/21	(66.7%)	2/34	(5.9%)	2/37	(5.4%)
Aguateca	0/3	(0.0%)	1/3	(33.3%)	4/4	(100.0%)	2/10	(2.0%)	0/11	(0.0%)
Tamarindito	0/3	(0.0%)	1/3	(33.3%)	1/4	(25.0%)	0/7	(0.0%)	0/8	(0.0%)
Itzán	1/1	(100.0%)	0/1	(0.0%)	1/1	(100.0%)	0/4	(0.0%)	0/4	(0.0%)
BELIZE ZONE										
Altun Ha	2/35	(5.7%)	24/27	(88.9%)	16/21	(76.2%)	3/41	(7.3%)	6/51	(11.8%)
Barton Ramie	0/16	(0.0%)	10/12	(83.3%)	5/8	(62.5%)	0/21	(0.0%)	0/19	(0.0%)
Baking Pot	0/1	(0.0%)	-----	-----	-----	-----	0/1	(0.0%)	0/1	(0.0%)
Colha	0/5	(0.0%)	3/4	(75.0%)	6/6	(100.0%)	0/13	(0.0%)	1/11	(9.1%)
SOUTHWESTERN ZONE										
Copan	1/17	(5.9%)	14/18	(77.8%)	10/12	(83.3%)	0/22	(0.0%)	0/25	(0.0%)
HIGHLANDS ZONE										
Kaminaljuyu	1/2	(50.0%)	1/2	(50.0%)	0/1	(0.0%)	0/14	(0.0%)	1/15	(6.7%)
PACIFIC COAST ZONE										
Balberta	0/3	(0.0%)	0/2	(0.0%)	-----	-----	0/2	(0.0%)	0/4	(0.0%)
Montana Complex	0/3	(0.0%)	1/3	(33.3%)	2/3	(66.7%)	0/5	(0.0%)	0/4	(0.0%)
COMBINED SAMPLE	15/284	(5.3%)	209/268	(78.0%)	130/186	(69.9%)	13/418	(3.1%)	18/429	(4.2%)

Table 6.5. Continued.

SITE	Torsomolar (LM3)		Cong. Abs. (LI1)		Cong. Abs. (LP4)		Cong. Abs. (LM3)	
CENTRAL ZONE								
Tikal	2/29	(6.8%)	0/91	(0.0%)	0/139	(0.0%)	4/104	(3.8%)
Tikal: Caches & Pr. Dep.	0/1	(0.0%)	0/10	(0.0%)	0/25	(0.0%)	1/23	(4.3%)
Uaxactun	1/3	(33.3%)	0/6	(0.0%)	0/8	(0.0%)	1/6	(16.7%)
Calakmul	1/2	(50.0%)	0/27	(0.0%)	0/33	(0.0%)	1/22	(4.5%)
USUMACINTA ZONE								
Piedras Negras	2/11	(18.2%)	0/47	(0.0%)	0/55	(0.0%)	1/42	(2.4%)
PASIÓN ZONE								
Altar de Sacrificios	0/6	(0.0%)	0/40	(0.0%)	0/49	(0.0%)	3/32	(9.4%)
Seibal	1/3	(33.3%)	0/24	(0.0%)	0/31	(0.0%)	3/15	(20.0%)
Dos Pilas	0/4	(0.0%)	0/31	(0.0%)	0/43	(0.0%)	2/35	(5.7%)
Aguateca	1/2	(50.0%)	0/10	(0.0%)	0/14	(0.0%)	0/9	(0.0%)
Tamarindito	0/2	(0.0%)	0/6	(0.0%)	0/8	(0.0%)	1/8	(12.5%)
Itzán	1/11	(9.1%)	0/4	(0.0%)	0/4	(0.0%)	0/4	(0.0%)
BELIZE ZONE								
Altun Ha	0/3	(0.0%)	0/54	(0.0%)	0/80	(0.0%)	0/38	(0.0%)
Barton Ramie	0/2	(0.0%)	0/27	(0.0%)	0/30	(0.0%)	0/17	(0.0%)
Baking Pot	0/2	(0.0%)	0/8	(0.0%)	0/5	(0.0%)	2/5	(40.0%)
Colha	0/8	(0.0%)	0/13	(0.0%)	0/19	(0.0%)	3/18	(16.7%)
SOUTHWESTERN ZONE								
Copan	1/4	(25.0%)	0/26	(0.0%)	0/37	(0.0%)	2/25	(8.0%)
HIGHLANDS ZONE								
Kaminaljuyu	0/2	(0.0%)	0/11	(0.0%)	0/24	(0.0%)	0/13	(0.0%)
PACIFIC COAST ZONE								
Balberta	1/2	(50.0%)	0/1	(0.0%)	0/4	(0.0%)	0/2	(0.0%)
Montana Complex	-----	-----	0/6	(0.0%)	0/7	(0.0%)	0/4	(0.0%)
COMBINED SAMPLE	10/89	(11.2%)	0/412	(0.0%)	0/570	(0.0%)	24/422	(5.7%)

Table 6.5 appears to indicate a general lack of patterning of dental trait frequencies within Maya archaeological zones. If there were strong isolation by distance in the Maya area, we should expect some trait frequencies to be similar within archaeological zones, and to differ between zones. However, this is not the case. One possibility is that substantial gene flow across the Maya prevented regional differentiation in dental traits. Alternatively, the apparent lack of patterning may simply reflect homogeneity in trait frequencies across the Maya area. Further statistical testing will determine whether significant differences in trait frequencies exist between Maya sites.

Log Likelihood Ratio Test

I calculated log likelihood ratio (G^2) tests to identify nonmetric dental traits that significantly varied between sites (Table 6.6). Traits with contingency tables that are comprised of more than 20% of the cells containing expected counts less than five were excluded from the analysis. Comparisons were made with the following sites: Tikal, Calakmul, Piedras Negras, Altar de Sacrificios, Seibal, Dos Pilas, Altun Ha, Barton Ramie, Colha, and Copan. Of the 28 traits included in the analysis, 14 exhibited statistically significant frequency difference between Maya sites. However, in a run of 28 G^2 tests, between 1 and 2 traits are expected to exhibit significant *p*-values (at the .05 level) due to familywise error alone. After adjusting for familywise error, four traits still exhibit statistically significant differences. Note that when Bonferroni's familywise error correction procedure was performed as an alternative to Šidák's single-step method, the same four traits were found to exhibit statistically significant frequency differences. Correcting for familywise error increases the risk of Type II error—failing to reject the null hypothesis in instances when it is false. However, if the adjusted and non-adjusted *p*-

Table 6.6. Log likelihood ratio tests (G^2) between sites for nonmetric traits with unadjusted *p*-values and *p*-values adjusted for familywise error with Šidák's single-step method.

	G^2	p	p_{adj}
Shoveling (UI1)	23.685	**0.003**	0.081
Shoveling (UI2)	17.888	**0.016**	0.363
Double Shoveling (UC)	32.503	**0.000**	**0.002**
Double Shoveling (UP3)	4.922	0.766	1.000
Int. Groove (UI2)	16.664	**0.034**	0.620
Tub. Dentale (UI1)	24.170	**0.002**	**0.054**
Tub. Dental (UI2)	18.873	**0.016**	0.363
Tub. Dentale (UC)	22.427	**0.004**	0.106
Metacone (UM1)	10.272	0.246	1.000
Metacone (UM3)	8.313	0.403	1.000
Hypocone (UM1)	21.389	**0.006**	0.155
Hypocone (UM2)	12.040	0.149	0.989
Lower Shoveling (UI1)	7.203	0.515	1.000
Premolar Cusp # (LP3)	44.260	**0.000**	**0.000**
Premolar Cusp # (LP4)	17.688	**0.024**	0.493
Anterior Fovea (LM1)	53.967	**0.000**	**0.000**
Anterior Fovea (LM2)	10.131	0.256	1.000
Groove Pattern (LM1)	11.764	0.162	0.993
Groove Pattern (LM2)	2.756	0.948	1.000
Cusp Number (LM1)	6.539	0.587	1.000
Def. Wrinkle (LM1)	16.585	**0.035**	0.631
Protostylid (LM1)	10.696	0.220	0.999
Protostylid (LM2)	20.206	**0.010**	0.245
Hypoconulid (LM1)	21.074	**0.007**	0.179
Hypoconulid (LM2)	6.457	0.596	1.000
Entoconulid (LM1)	5.081	0.749	1.000
Tomes' root (LP3)	8.625	0.435	1.000
Enamel Ext. (LM2)	11.009	0.201	0.998

values are considered as a minimum and maximum range, between 14% and 50% of the dental nonmetric traits exhibit statistically significant differences between Maya sites. These results indicate moderate levels of dental heterogeneity in the Maya area.

Mean Measure of Divergence

I based the MMD analysis on a final set of 23 dental nonmetric traits (Table 6.4). It is advised that the MMD analysis be run with relatively large sample sizes, with ten observations per trait a recommended minimum sample size. I calculated a MMD matrix using the following sites: Tikal, Calakmul, Piedras Negras, Altar de Sacrificios, Seibal, Dos Pilas, Altun Ha, Barton Ramie, Colha, Copan, and Kaminaljuyu (Table 6.7). However, the following sites have more than 25% of their traits under a sample size of ten: Kaminaljuyu (n = 7), Colha (n = 7), Copan (n = 5). Thus, any distance value incorporating these sites must be treated with caution and I performed cluster and multidimensional scaling analyses both with and without these problematic sites.

The smallest pairwise values are negative values between Barton Ramie and Altun Ha (-0.8141) and Copan and Barton Ramie (-0.4768). In reality, it is impossible for two sites to have biological distances of less than 0, since 0 is identity. Rather, the negative values are a result of the modifications to the MMD statistic to control for small sample size. Nevertheless, these small pairwise values indicate biological similarity between the sites. On one hand, this relationship could indicate a true biological affinity, especially in the case of Altun Ha and Barton Ramie, which are geographically close to one another. Alternatively, small sample sizes could be affecting the results. For the site of Kaminaljuyu, although it is intriguing to suggest the relatively low pairwise distances are indicative of gene flow with the lowland sites, its

Table 6.7. Standardized Mean Measure of Divergence matrix for Classic period samples.

	Tikal	Calakmul	P. Negras	Altar	Seibal	Dos Pilas	Altun Ha	B. Ramie	Colha	Copan
Calakmul	**3.6610**[1]	----								
P. Negras	**3.2602**	**6.1324**	----							
Altar	**8.6802**	**3.5705**	**9.6632**	----						
Seibal	**5.3689**	**2.7687**	**7.4437**	0.4384	----					
Dos Pilas	**4.0353**	**3.5297**	**4.1896**	**7.7630**	**7.6935**	----				
Altun Ha	**7.9607**	**2.0485**	**7.5868**	**5.9627**	**3.8655**	**5.3680**	----			
B. Ramie	**3.7625**	0.1975	**5.0489**	**2.3021**	1.9847	1.8507	-0.8141	----		
Colha[2]	**3.7197**	**7.9422**	**3.3011**	**9.2810**	**7.4035**	**4.3744**	**9.9129**	**8.2345**	----	
Copan[2]	**3.9724**	0.0577	**7.5139**	**2.4605**	1.0122	**2.9334**	1.4096	-0.4768	**8.2647**	----
Kaminaljuyu[2]	0.3444	0.4481	**3.0787**	**4.3820**	**3.8280**	0.6839	0.7383	0.0135	**3.3990**	0.1062

[1]Values in bold are statistically significant.
[2]More than 25% of traits have sample size < 10.

problematic sample size may be affecting the results. More interesting, is the small pairwise distance between the sites of Altar de Sacrificios and Seibal (0.4383). These sites are geographic neighbors and archaeologically demonstrate a cultural affinity, such that a biological relationship would be expected. Of note are the generally large pairwise distances between the site of Piedras Negras and the other sites in the study (3.0787 to 9.6632). Archaeological and epigraphic data indicate that Piedras Negras had a strong affinity to other sites in the greater Usumacinta area (Yaxchilan, Pomona, Tonina, Palenque) and much less so to other parts of the Maya area. Thus, it is not surprising that Piedras Negras appears biologically distinct from the other sites in the study.

When the pairwise distance values are considered as a whole, it is evident that most of the distances (40/54, 74.1%) are larger than 2.0, indicating significance at the 0.05 level (Sjøvold 1973). These results point towards substantial heterogeneity in dental nonmetric traits within the Maya area, as originally indicated in the univariate comparisons.

In order to determine whether there was an association between the MMD distance matrix and geographic distance in the Maya area, I performed a Mantel test. The Mantel test determines whether there is a significant correlation between two data matrices. The geographic distance matrix was the independent matrix in the analysis (Table 6.8). I measured geographic distances as the smallest distance between two Maya sites, in kilometers. Of course, these distances do not measure the true routes of travel between Maya sites. For instance, the primary routes of travel in the Usumacinta and Pasión Zones were likely the major river systems and adjacent valleys, rather than direct courses over land. However, Maya transport routes are poorly understood and any effort to incorporate them into the geographic distance matrix would be guesswork at best. Nonetheless, when taken for the Maya area as a whole, the geographic distances used here are good approximations of the length of travel between Maya sites,

Table 6.8. Direct geographic distance between Maya sites (km)

	Tikal	Calak-mul	Piedras Negras	Altar	Seibal	Dos Pilas	Altun Ha	Barton Ramie	Colha	Copan	Kaminal-juyu
Calakmul	100										
Piedras Negras	175	180									
Altar	125	200	110								
Seibal	90	180	145	50							
Dos Pilas	110	190	125	25	25						
Altun Ha	150	160	315	275	230	250					
Barton Ramie	70	130	240	180	140	165	90				
Colha	160	155	315	285	250	170	30	105			
Copan	275	370	340	230	205	220	340	270	370		
Kaminal-juyu	315	400	300	215	225	215	425	345	450	150	
Pacific[1] Coast	375	470	350	275	290	275	500	415	520	200	70

[1]Measured from the site of Balberta, Guatemala

regardless of the exact route used. Note that Table 6.8 also includes geographic distances from the Pacific Coast, which is used in the dental metric statistical tests, but not in the nonmetric analyses.

The following results were obtained for the Mantel test of correlation between geographic distance and MMD distance in the Maya area: $r = -0.1953$; $r^2 = 0.0382$; $p = .8230$. There is clearly no correlation between geographic distance and the MMD distance values. In fact, the *r* value indicates the trend, though not significant, is for MMD distance to *decrease* as geographic distance increases. These results are contrary to the expectations of an isolation by distance model, in which biological distance should increase with geographic distance.

To better understand the patterning of biological distance in the Maya area, I derived a dendogram from the standardized MMD values (Figure 6.1). The challenge of interpreting dendograms is identifying a point along the tree in which the clusters are meaningful for the analysis. On the far left of the dendogram, all samples are a separate cluster, on the far right; all samples are joined to a single cluster. In Ward's method, joining proceeds in an order that minimizes cluster variability based on a Sum of Squares. As a hierarchical agglomerative technique, I am more or less free to choose the level of clustering. I have selected a point that recognizes three major branches: (1) Barton Ramie-Copan-Kaminaljuyu-Calakmul-Altun Ha, Dos Pilas, (2) Altar-Seibal, and (3) Tikal-Piedras Negras-Colha. By dividing the clusters at this point, I am drawing a distinction between the small and large branches.

The overall picture of intersite heterogeneity is underscored in the dendogram. With the exception of the Altar-Seibal cluster, sites do not cluster with fellow members of their respective archaeological zones. Particularly unusual is the close relationship between Barton Ramie, Copan, Kaminaljuyu, and Calakmul. An association between Copan and Kaminaljuyu would

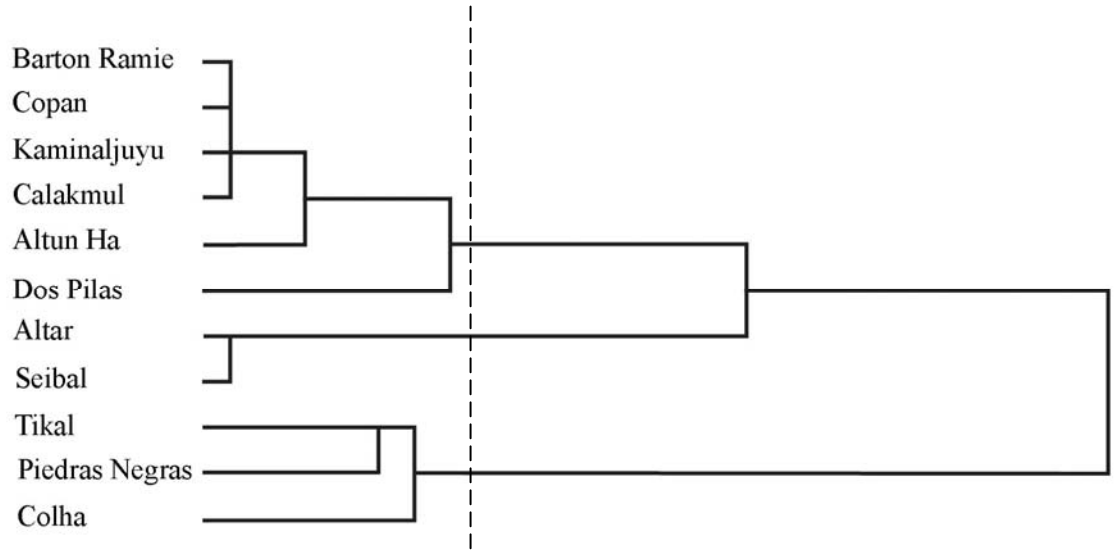

Figure 6.1. Cluster analysis of Classic period MMD distances. Dashed line divides dendogram into clusters discussed in text.

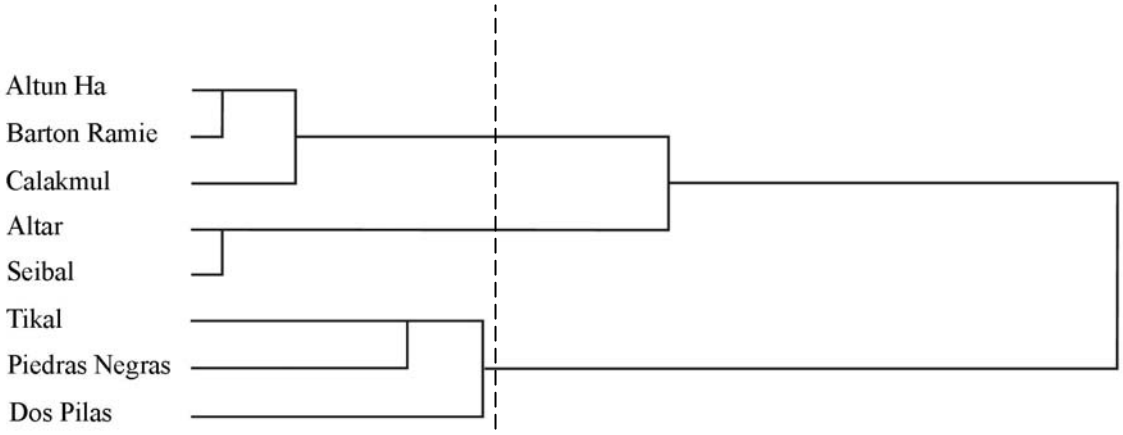

Figure 6.2. Cluster analysis of Classic period MMD distances, excluding sites with problematic sample sizes. Dashed line divides dendogram into clusters discussed in text.

not be surprising due to their geographic proximity and evidence of cultural material exchange (Bell, et al. 2004; Reents-Budet, et al. 2004). The association with Calakmul and these sites, however, does not fit isolation by distance nor is it readily explained by any current archaeological or historical models. Rather, this clustering of sites is more likely a product of problematic sample size, as already noted.

I constructed a second dendogram, excluding the sites with problematic sample sizes (Figure 6.2). For the most part, the second dendogram is similar to the first. The most notable difference is that Altun Ha and Barton Ramie now join on a small branch of the dendogram, along with Calakmul. As with Figure 6.1, Altar and Seibal cluster together on a second branch. The third major branch includes Dos Pilas, Piedras Negras and Tikal, though the clustering of these three is very loose. What is interesting is that the dendogram in Figure 6.2 more closely approximates what is known about the interactions between these sites from the archaeological and historical record. As already mentioned, the clustering of the Pasión sites of Altar de Sacrificios and Seibal was expected. Similarly, the biological affinity between the Belizean sites of Altun Ha and Barton Ramie is not surprising. The third major branch is comprised of the distantly related sites of Tikal, Dos Pilas, and Piedras Negras. Although this affiliation is very loose, this cluster may reflect ancient historical events, particularly the founding of the dynasty at Dos Pilas by members of the Tikal ruling family (Houston 1993; Martin and Grube 2000).

An undesirable aspect of cluster analysis is that readers have a tendency to interpret the dendogram much like a family tree, with each successive branch representing a new division in an historical lineage with a common origin. Thus, I have chosen to re-plot the MMD values using multidimensional scaling (MDS). I have plotted both the full set of pairwise distances (Figure 6.3) and a sub-set that excludes the sites with problematic sample sizes (Figure 6.4). The

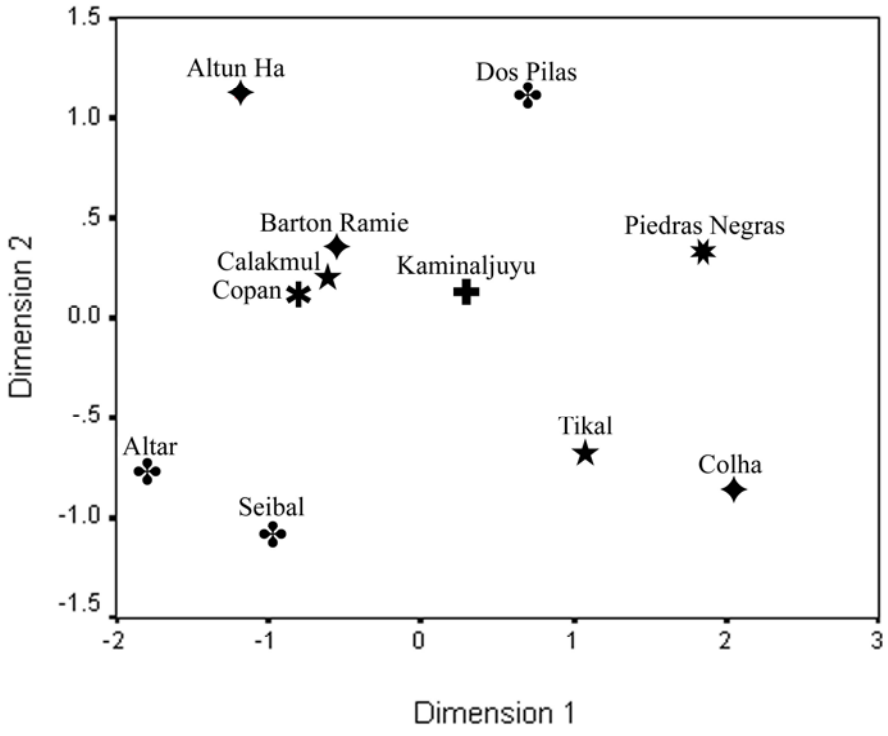

Figure 6.3. Multidimensional scaling of Classic period MMD distances. Archaeological Zones: Central (★), Pasión (✤), Usumacinta (✸), Belize (✦), Southeast (✱), Highlands (✚).

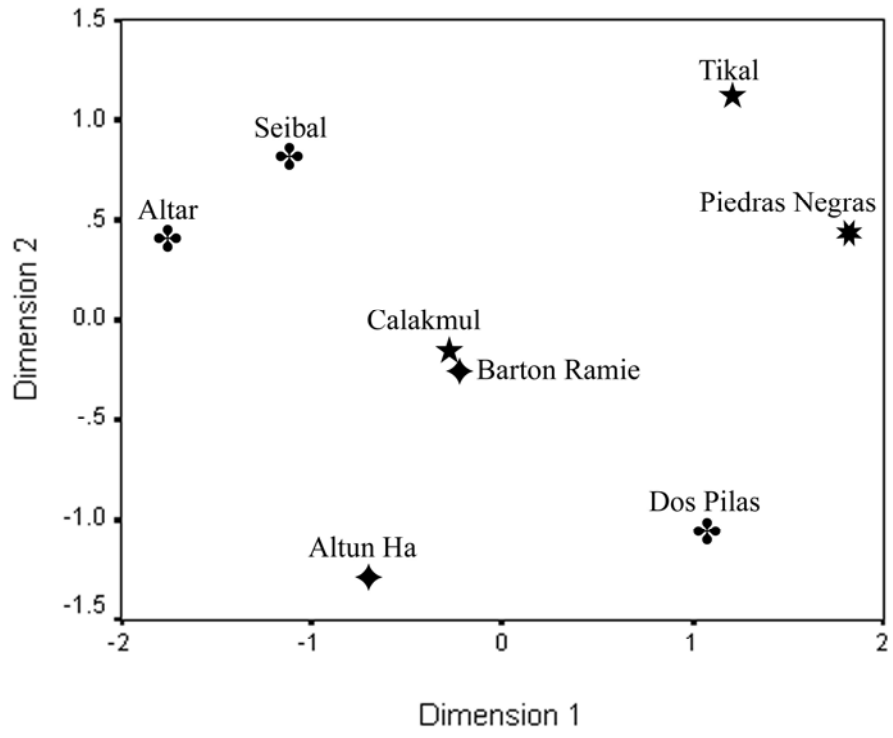

Figure 6.4. Multidimensional scaling of Classic period MMD distances, excluding sites with problematic samples sizes. Archaeological Zones: Central (★), Pasión (✤), Usumacinta (✸), Belize (✦).

resulting MDS plots show essentially the same relationships that are illustrated in the cluster analysis. The main difference is that Barton Ramie is plotted closer to Calakmul in the MDS plot with the reduced list of sites (Figure 6.4), while in the corresponding cluster analysis (Figure 6.2); Barton Ramie is clustered with Altun Ha. This is due to differences in the methods of cluster analysis and multi-dimensional scaling. Cluster analysis is a stepwise procedure that attempts to minimize within-cluster variation while maximizing between-cluster variation. By contrast, multidimensional scaling simultaneously considers all distance values for a best fit in Euclidean space. If we refer back to the original distance matrix, the Barton Ramie-Calakmul pairwise distance is actually greater than that between Barton Ramie and Altun Ha.

What is most evident in the MDS plot, and less apparent in the cluster analysis, is the relative lack of clustering between Maya sites. If we consider the plot without the sites with problematic sample sizes (Figure 6.4), the only evident cluster is that of Barton Ramie and Calakmul. The remaining sites are widely scattered across the plot, with most plotted away from the centroid. A loose association is found between Altar de Sacrificios and Seibal, as well as between Tikal and Piedras Negras. In the case of Altar and Seibal, this is due to a small pairwise distance between the two (0.4384). However, in the case of Tikal and Piedras Negras, this association is more a product of the two sites' lack of affinity with any other site (all MMD values are significant) than it is due to a strong affinity between the two. Although Tikal's smallest distance is with Piedras Negras, it is not a particularly small distance (3.2602).

Unfortunately, interpreting the results of the MMD analysis is far more complex than simply assuming that sites with small pairwise distance values correlate with close biological affinity. In reality, a complex interplay of genetic drift and gene flow may be clouding our ability to elucidate population history in the Maya area. Thus, I will reserve further discussion of

the significance of these findings for Chapter VIII, where the nonmetric data can be considered in concert with the metric data, as well as the archaeological and epigraphic record.

SUMMARY

I collected dental nonmetric data for 987 individuals from 18 sites in the Maya area. Univariate analysis of the dental nonmetric data found substantial heterogeneity in trait frequencies between Maya sites. Using a subset of 24 dental nonmetric traits from 11 Maya sites, a multivariate Mean Measure of Divergence analysis demonstrated that the majority intersite distances were statistically significant. A Mantel test of the standardized MMD values found a lack of association between biological and geographic distance. The cluster analysis generated clusters that were only moderately similar to those expected under an isolation by distance model. The multidimensional scaling plots further underscored the heterogeneity among Maya sites and the lack of regional association between Maya sites.

CHAPTER VII

DENTAL METRIC ANALYSES

In this chapter I review the methods and result of my analysis of Classic Maya dental metric variability. This summary includes a description of (1) the procedures used to collect the data, (2) the statistical methods used to examine ancient Maya population variability, and (3) the results of those analyses.

DATA COLLECTION

I collected dental metric data using a pair of Mitituyo digital pointed jaw calipers. I used the same calipers to collect all of the metric data in this study. I took mesiodistal and buccolingual measurements following the methodology of Moorrees (1957) and Wolpoff (1971), which has become the standard for bioarchaeological studies (Buikstra and Ubelaker 1994). In this method, the mesiodistal measurement is taken as the maximum length in the mesiodistal plane. This is different than the methodology of Goose (1963), which is occasionally used in dental metric studies. In this approach, the mesial and distal interstitial contact points are used to obtain mesiodistal length. I measured buccolingual breadth as a maximum measurement perpendicular to the mesiodistal length. I measured maximum crown height as a maximum measurement from the cemento-enamel junction to the occlusal surface on the buccal surface. However, I did not use this measurement in this study, since even minor wear affects its accuracy. In order to ensure accuracy, I measured each metric trait three times before recording it.

Occlusal and interstitial dental wear, calculus, caries, and artificial modification can all affect the accuracy of dental measurements. As a result, I treated any measurement that was

even suspected of being affected by one of these factors as missing data. Fortunately, the most serious factor inhibiting the collection of metric data, dental wear, is relatively minor among the ancient Maya (Glassman and Garber 1999; Scherer, et al. 2004). As a result, sample sizes were not as seriously reduced by wear as they often are in ancient populations from other parts of the world. In some studies, dental wear led researchers to use cervical crown measurements (Powell 1995), a procedure that was not followed here.

As discussed for nonmetric traits, the pooling of data from antimeres in dental studies of biological distance can inaccurately inflate sample size for some individuals, thus biasing the results. Therefore, I used only measurements for the left teeth for statistical analyses. However, in order to maximize sample size, when the left measurement was missing, I substituted data from the right tooth, a standard procedure in dental metric studies (e.g., Powell 1995; Rhoads 2002; Stojanowski 2001).

Measurement Elimination

As with the dental nonmetric traits, it is necessary to determine if any error was introduced into the dental metric analysis by intraobserver error. Discordance may be the result of error in the calipers, observer fatigue, or changes in measurement practices. Although only one set of calipers was used to collect all of the data in this study and every effort was made to minimize fatigue while collecting data, it remains possible that error was introduced through the course of data collection from subtle changes in measuring technique. Thus, it is imperative to test for intraobserver error in this analysis.

I tested intraobserver error on a subset of 10 individuals from the site of Altun Ha, separated by a time period of one week. First, a paired Student's *t*-test was performed to determine if there was any systematic error in the scoring procedure between the first and second

data collection sessions (Kieser 1990: 14). Table 7.1 lists the results of this analysis. None of the mesiodistal or buccolingual measurements demonstrated significant error at the 0.05 significance level. The mean intraobserver error (all measurements combined) was .037 mm (s.d. = .047), a difference that is comparable to that found in other studies (Lukacs and Hemphill 1991; Powell 1995; Stojanowski 2001). Based on these results, intraobserver error is not a significant problem in this study for any of the trait-measurement combinations.

Many of the multivariate statistics for metric data used to analyze ancient population history require that the data are normally distributed. I tested for normality for each measurement with the Kolmogorov-Smirnov test and using Lilliefors significance test in SPSS. I performed these tests using a combined dental sample from all sites in the analysis. The results of this test are in Table 7.1. In general, mesiodistal measurements tended to be more normally distributed than buccolingual measurements. This is likely due to the fact that a number of buccolingual measurements can be affected by the presence of accessory cusps and other nonmetric traits on the cingulum of the anterior teeth and on the labial and lingual surfaces of the molars. Four buccolingual measurements were found to be non-normally distributed: UM2BL, UM3BL, LCBL, and LM3BL. I eliminated these measurements from the multivariate analyses.

Unlike the skeleton, the dentition does not remodel during life. Thus, we would not expect the measurements of teeth to vary between adults and subadults. However, two factors could produce variability in tooth dimensions between individuals of different ages. First, research has shown that, within some populations, individuals who died as subadults have smaller dentition than those who died as adults (Guagliardo 1982; Simpson, et al. 1990).

Table 7.1. Test of intraobserver error, normality, and age influence on dental measurements.

	Test of Intraobserver Error		Test of Normality	Test of Age Influence
Tooth Measure	**Mean Absolute Difference**	***t*-test (*p*)**	**Kolmogorov-Smirnov (*p*)**	***F* (*p*)**
UI1MD	.004	-.478 (.649)	.036 (.200)	.014 (.906)
UI1BL	.000	.000 (1.000)	.037 (.200)	.002 (.962)
UI2MD	.010	.764 (.474)	.050 (.096)	1.009 (.317)
UI2BL	.022	-.910 (.414)	.042 (.200)	**5.459 (.020)**[1]
UCMD	.001	.146 (.886)	.031 (.200)	.072 (.789)
UCBL	.018	-2.037 (.069)	.026 (.200)	.109 (.742)
UP3MD	.005	-1.254 (.236)	.025 (.200)	**7.267 (.007)**
UP3BL	.005	-0.239 (.816)	.031 (.200)	.125 (.723)
UP4MD	.016	-2.058 (.070)	.041 (.083)	**4660 (.032)**
UP4BL	.010	-0.733 (.484)	.034 (.200)	.138 (.711)
UM1MD	.031	.504 (.628)	.033 (.200)	.692 (.406)
UM1BL	.034	.669 (.520)	.019 (.200)	.875 (.350)
UM2MD	.029	-2.248 (.055)	.026 (.200)	2.160 (.143)
UM2BL	.006	-.393 (.705)	**.043 (.048)**	.004 (.951)
UM3MD	.008	.595 (.578)	.040 (.200)	.007 (.935)
UM3BL	.002	-.133 (.899)	**.094 (.000)**	.188 (.665)
LI1MD	.010	1.369 (.229)	.061 (.083)	.370 (.544)
LI1BL	.008	.140 (.895)	.056 (.094).	.696 (.405)
LI2MD	.003	-.378 (.742)	.036 (.200)	**5.018 (.026)**
LI2BL	.052	2.414 (.095)	.043 (.200)	.300 (.585)
LCMD	.002	-.210 (.842)	.030 (.200)	.267 (.606)
LCBL	.077	.867 (.477)	**.052 (.036)**	.325 (.569)
LP3MD	.025	1.015 (.330)	.033 (.200)	1.831 (.177)
LP3BL	.022	-.768 (.462)	.041 (.069)	2.226 (.137)
LP4MD	.021	-1.538 (.168)	.032 (.200)	**6.119 (.014)**
LP4BL	.056	1.910 (.098)	.027 (.200)	3.323 (.069)
LM1MD	.007	-0.633 (.539)	.025 (.200)	2.955 (.087)
LM1BL	.033	1.245 (.237)	.029 (.200)	.659 (.418)
LM2MD	.005	0.428 (.676)	.024 (.200)	1.183 (.278)
LM2BL	.045	-1.150 (.273)	.037 (.171)	4.075 (.055)
LM3MD	.012	-0.158 (.882)	.029 (.200)	.830 (.363)
LM3BL	.016	-.309 (.773)	**.050 (.048)**	1.278 (.260)

[1]Bold items are significant at $p < .05$.

That is, individuals who die as subadults were subjected to higher levels of physiological stress, or were inhernently frailer, than those who died as adults. In either case, it is expected that these individuals might have a reduction of tooth size relative to those individuals who were in relatively good health. Dental wear is another factor that might produce differences in adult and subadult dental dimensions. Although I made every effort to only measure teeth with little to no attrition, it is possible that tooth size in adult individuals may have been affected by interstitial wear.

To test for the possible influence of age on tooth dimensions, I performed a linear regression analysis with each measurement regressed on age. I used the median age of each age category was used for this analysis. This analysis was performed on a combined dental sample. Table 7.1 indicates that three mesiodistal measurements (UP3MD, UP4MD, LI2MD, LP4MD) and one buccolingual measurement (UI2BL) were found to exhibit an association with age. I excluded these measurements from any multivariate analyses.

I also included all maxillary and mandibular third molar measurements. Research has demonstrated that the third molar is most subject to environmental effects (Taylor 1978), thus third molar measurements are not suitable for reconstruction of ancient population history. Further, since third molars are formed during later adolescence, they can only be measured in older individuals.

Missing Values

Most multivariate statistics used on dental metric data require complete data matrices. However, it is rare that all measurements are available for a given individual, especially in this study, which relies on fragmentary Maya skeletal remains. One option is to eliminate all of the cases with missing data. Unfortunately, this approach will eliminate nearly all of the cases in the

analysis. Another option is to replace the missing values with the site mean for each measurement. However, this approach will reduce intra-group variance and quite possibly between-group differences as well. A final option is to estimate the missing data. I take this approach here, which is common in studies of prehistoric population differences (Key 1982; Powell 1995; Rhoads 2002; Stojanowski 2001).

I chose to estimate the missing data through a method known as multiple imputation. Multiple imputation is the practice of filling in missing data with a series simulated values and then combining the results to minimize missing data uncertainty (Schafer 1999a). I began the process of data imputation with the reduced list of traits, after removing the measurement that were non-normally distributed or demonstrated an association with age. One must be cautious when estimating missing values in order to prevent estimating the majority of the data that will be used in the statistical analysis. I removed individuals from the dataset who had too few measurements and removed measurements that were taken on too few individuals. The initial dataset consisted of 905 individuals, for whom 55.1% (10490/19005) of the measurements are missing. Of these 905 individuals, a mean of 389.5 individuals could be measured for a particular measurement. However, when each measurement was considered separately, it is clear that the anterior teeth yielded a particularly low number of observable individuals (~200/per trait), in comparison to the measurements of the posterior teeth which yield between 400 and 500 hundred individuals per measurement. First, I removed all sites with problematic sample sizes. Next, I removed measurements and individuals from the remaining sites in a stepwise fashion to achieve a balance where no more than one third of the measurements for any individual were estimated. Thus, I reduced the dataset to 352 individuals and nine measurements. Table 7.2 lists the traits that were considered before imputation and the final list of traits that were subjected to imputation after I removed measurements with low

Table 7.2. Metric traits considered before data imputation and the final nine traits used in data imputation and subsequent multivariate analyses.

Pre-Imputation	Traits Included for Imputation
UI1MD	
UI1BL	
UI2MD	
UCMD	
UCBL	
UP3BL	Included
UP4BL	
UM1MD	Included
UM1BL	Included
UM2MD	
LI1MD	
LI1BL	
LI2BL	
LCMD	
LP3MD	Included
LP3BL	
LP4BL	Included
LM1MD	Included
LM1BL	Included
LM2MD	Included
LM2BL	Included

sample sizes.

In order to estimate missing values, I used NORM, a multiple imputation program (Schafer 1999b). NORM generates multiple imputations of the data by using a data augmentation algorithm (Schafer 1999a). These multiple imputations are then combined using Rubin's rules for scalar estimands (Rubin 1987). In order to run the imputation procedure, NORM requires the data are normally distributed. Although the data was already tested for normality, I retested for normality since many individuals with missing data had been removed from the dataset since I performed the original test of normality. All of the measurements shown in the second column of Table 7.2 were found to be normally distributed and thus ready for data imputation.

After data imputation was complete, I compared the original data to the imputed data using *t*-tests and *F*-tests to determine if there were any statistically significant differences between the means and variances of the original and imputed data. Table 7.3 shows that there is neither a statistically significant difference in the variances (*F*-test) nor the means between the pre-imputation and post-imputation datasets. As a further test of the reliability of imputation, I performed five separate multiple imputation runs. I compared the means of each of these five runs to one another using ANOVA. In this analysis, I excluded the original data so that only the imputed data was being compared in ANOVA. Table 7.4 lists the results of the ANOVA. Again, no statistically significant differences were found. I performed an additional test of the reliability of data imputation during **R** matrix analysis and I discuss those results in that section of this chapter.

Table 7.3. *F*-test and *t*-test comparing pre-imputation and post-imputation datasets.

Measurement	***F*** **(*p*)**	***t*** **(*p*)**
UP3BL	0.128 (0.720)	-0.114 (0.910)
UM1MD	0.185 (0.667)	0.243 (0.808)
UM1BL	0.011 (0.915)	-0.162 (0.871)
LP3MD	0.011 (0.918)	-0.624 (0.533)
LP4BL	0.183 (0.669)	-0.262 (0.793)
LM1MD	0.115 (0.734)	0.025 (0.980)
LM1BL	0.006 (0.936)	0.106 (0.916)
LM2MD	0.145 (0.704)	-0.204 (0.838)
LM2BL	0.088 (0.766)	-0.078 (0.938)

Table 7.4. ANOVA comparing five different dental measurement imputations.

Measurement	***F*** **(*p*)**
UP3BL	0.144 (0.966)
UM1MD	1.570 (0.182)
UM1BL	0.774 (0.543)
LP3MD	0.169 (0.954)
LP4BL	0.089 (0.986)
LM1MD	0.831 (0.508)
LM1BL	0.579 (0.678)
LM2MD	0.543 (0.704)
LM2BL	0.122 (0.975)

Sex Effects

The dimensions of human teeth are known to be sexually dimorphic (Arya, et al. 1974; Black 1978; Ditch and Rose 1972; Garn, et al. 1964; Potter 1972). The ancient Maya are no exception. Table 7.5 illustrates the mean differences in male and female tooth measurements from the total sample. I found the sexes exhibited statistically significant different mean dental dimensions for 75% (15/20) of the measurements considered (excluding measurements that demonstrated an age affect or were not normally distributed). Although these results are clearly subject to familywise error, they nonetheless underscore the sexual dimorphism present amongst the ancient Maya.

In the distribution of sex in the Classic period sample, males tend to outnumber females 2:1 (Table 5.1). This bias may be the result of a number of factors. One possibility is random sampling error. For instance, at Piedras Negras I found that males and females were evenly distributed in the total skeletal sample even though there is apparently a sex bias in the dental sub-sample (Scherer, et al. 2004). However, Wright (1994: 95) reports sex bias in the skeletal samples throughout the Pasión sites. This suggests that there is in fact a sex bias in at least some Maya skeletal samples. One explanation is that the Maya may not have buried males and females in the same locations. This may be particularly true for the monumental core of sites where the majority of prehistoric public ritual and, thus, archaeological activity occurs.

An additional problem is the probability of a low accuracy of sex determination as a result of poor skeletal preservation in the Maya area. As a result, it is often impossible to sex skeletons by multiple skeletal indicators, and in particular, the pelvis—the most reliable indicator of sex—is only rarely preserved. In order to circumvent this problem, some researchers have turned to discriminant function analysis of long bones and teeth to sex skeletons (Whittington 1989; Wright 1994; Wrobel 2003). The concern with this approach is that the "known" sex

Table 7.5. Total Classic period male and female mean tooth size and t-test.

Tooth Measure	Males			Females			t (p)
	N	Mean	s.d.	N	Mean	s.d.	
UI1MD	44	8.803	.507	28	8.809	.609	-0.048 (.961)
UI1BL	87	7.456	.503	59	7.169	.455	3.520 (.001)
UI2MD	54	7.273	.712	54	7.273	.712	0.590 (.556)
UCMD	91	8.433	.495	64	8.040	.418	5.178 (.000)
UCBL	105	8.820	.676	77	8.235	.468	6.533 (.000)
UP3BL	115	9.671	.702	69	9.315	.563	3.578 (.000)
UP4BL	115	9.506	.722	69	9.253	.617	2.433 (.016)
UM1MD	72	11.091	.563	61	10.802	.603	2.856 (.005)
UM1BL	80	12.111	.597	65	11.770	.525	3.603 (.000)
UM2BL	87	12.055	.851	65	11.512	.576	4.443 (.000)
LI1MD	33	5.680	.392	25	5.684	.341	-0.037 (.971)
LI1BL	42	5.804	.385	34	5.704	.289	1.251 (.215)
LI2BL	64	6.253	.429	48	6.170	.347	1.088 (.279)
LCMD	79	7.359	.435	66	7.032	.376	4.786 (.000)
LP3MD	104	7.184	.504	76	7.032	.434	2.111 (.036)
LP3BL	96	8.111	.566	70	7.838	.467	3.303 (.001)
LP4BL	109	8.502	.631	75	8.228	.525	3.095 (.002)
LM1MD	92	11.888	.451	59	11.661	.564	2.739 (.007)
LM1BL	87	11.031	.537	64	10.762	.502	3.124 (.002)
LM2MD	95	11.365	.736	62	11.104	.739	2.168 (.032)
LM2BL	91	10.587	.600	63	10.266	.535	3.408 (.010)

sample (where sex is determined by macroscopic indicators of the os coxa and cranium) is often quite small. Although it is impossible to verify the accuracy of sex estimation in the Maya lowlands, this is a concern, nonetheless, and could partially explain the bias in sex observed in some skeletal samples.

There are two options available deal with individuals of indeterminate sex. I could either (1) combine the sexes for analysis or (2) perform a discriminant function to estimate sex from "known" individuals. The second approach has been employed in other anthropological studies of dental metric variation (Stojanowski 2003b). However, such a method may not be reliable in cases where the majority of individuals are of indeterminate sex, as in this study. Further, if discriminant analysis were used here, it would be inevitable that some of the individuals of "known" sex cases are actually individuals for which sex was determined through discriminant function analysis by earlier researchers. Thus, I have chosen to pool sexes. Assuming that there is a true bias in sex in the samples in this study, rather than major inaccuracies of sex determination between different researchers, the bias appears to be more or less consistent across the samples (Table 5.1). In this case, the male versus female contribution will be equal across the samples. Both Wrobel (2003) and Rhoads (2002) followed this approach in their analyses of dental metric variability amongst the Maya samples they examined.

Dental Shape

Research on dental metrics has demonstrated that size is a poor indicator of biological affinity as a result of allometric affects (Corruccini 1973; Kieser 1990; Perzigian 1984). One method for working around this issue involves partitioning the data into size and shape components (Penrose 1954). Alternatively, size can be removed by dividing the dental

measurements by an individual reference variable (Corruccini 1973; Darroch and Mosimann 1985). I follow the latter approach here.

I used a Q-mode correction of the data, as suggested by Corrucini (1973). In this approach, an individual size reference variable is determined for each skeleton in the study. For each case, the geometric mean for all of the measurements of that individual is used as the reference variable. Each measurement is divided by this reference variable. This approach has been applied in both craniometric (Neves and Pucciarelli 1991; Powell and Neves 1999; Steele and Powell 1992, 1993) and dental metric studies (Powell 1995). In order for this approach to work, a complete data set is necessary. Thus, Q-mode correction was performed on the nine variables for which imputed data was available. The benefit of Q-mode correction is that not only does it eliminate any allometric factor that might be influencing tooth size; it should also negate the size differences between individuals resulting from sexual dimorphism.

STATISTICAL METHODS

Unlike the dental nonmetric data, the metric data readily lend themselves to model-bound analyses of population history. Thus, I have opted to use both model-free and model-bound approaches. Model-free approaches are selected because they (1) rely on few theoretical assumptions and are thus relatively easy to compute, (2) provide a useful heuristic device for determining general patterns of biological variability and (3) they are the most widely used statistics for analyzing ancient population variability. In contrast, model-bound approaches incorporate additional population parameters and thus theoretically should be provide more accurate reconstructions of population history. However, some of the parameters in model-bound approaches—most notably population size—cannot be derived empirically but must be

estimated. This could create error in the analysis. Therefore, I will use both approaches and carefully assess the similarities and differences in the results.

Analysis of Variance and Covariance

In order to test for inter-site differences in the means and variances of dental measurements, I performed univariate analyses of variance (ANOVA) and multivariate analyses of variance (MANOVA). ANOVA permits testing differences between sample means by following the same general procedure as regression analysis (Field 2000). ANOVA, which is synonymous with the *F*-test, is calculated by comparing the variance between samples

$$F = s_{bg}^2 \Big/ s_w^2$$

where s_{bg}^2 is the between-group variance and s_w^2 is the within-group variance. As such, *F* values significantly larger than 1 indicate that the compared means are statistically different. Since ANOVA compares the sample means in a single analysis, the potential for familywise error inherent in running multiple *t*-tests is avoided.

In addition to ANOVA, I performed Levene's (1960) test to determine if the variances of the different sites different sites were significantly different. The equation for Levene's test is

$$W = \frac{(N-k)}{(k-1)} \frac{\sum_{i=1}^{k} N_i \left(\overline{Z}_{i,} - \overline{Z}_{,,}\right)^2}{\sum_{i=1}^{k} \sum_{j=1}^{N_i} \left(Z_{ij} - \overline{Z_{i,}}\right)^2}$$

where *N* is the total sample size, $Z_{ij} = \left|Y_{ij} - \overline{Y_{i,}}\right|$ where $Y_{i,}$ is the mean of the *i*th sample, and *k* is the number of samples. Thus, Levene's test not only informs about the variability in dental measurements between Maya sites, but is also relevant for checking the validity of the ANOVA

analysis, which requires homogenous variances across the samples in the analysis. Levene's test is particularly appropriate here as it is robust in situations where the data are not normally distributed (Manly 1994), which is potentially a problem in this study due to the small sample sizes of some sites.

MANOVA is much like ANOVA, but considers multiple variables, in addition to multiple samples in the analysis of variance. SPSS 11.5.0 calculates MANOVA through the Generalized Linear Model Procedure. A number of procedures are available for calculating *F* ratios in this package. I elected to use the relatively conservative Wilk's λ for this analysis.

Principal Components Analysis

Principal Components Analysis (PCA) provides a relatively simple multivariate approach for examining patterns of dental metric differences between Maya sites. PCA is a data reduction technique that generates new variables (the principal components) from the original dataset. The principal components are derived from the orthogonal vectors of the pooled variance-covariance matrix of the total Classic period dataset (Manly 1994). The principal components are ranked by the amount of the total variance that they explain. Typically, the first two or three principal components explain the majority of the total variance. As a result, it is possible to reduce the original list of metric variables to a series of principal components that can easily by plotted and compared. Since phenotypic covariance is related to genetic covariance (Chevrud 1988; Konigsberg and Ousley 1995; Williams-Blangero and Blangero 1989), PCA can be used to analyze population differences between Maya sites. Sites that occupy the same space in the PCA plots possess similar dental dimensions and are thus are genetically similar, to some degree.

I performed PCA on the complete, Q-mode transformed, imputed dataset. Principal components were derived for each individual in the dataset. Mean principal component values were then derived for the first three principal components for each site-sample. The principal component centroids for each site are then plotted in three dimensional space.

Mahalanobis Distance

Perhaps the most commonly employed multivariate statistic to calculate biological distance from metric data is Mahalanobis distance statistic, D^2 (Mahalanobis 1936). The popularity of Mahalanobis distance is due to its relative ease of computation and its ability to control for correlation of variables in the analysis. This is particularly important for the analysis of dental metric data for which there are demonstrated intertrait correlations in tooth dimensions (Garn, et al. 1965a, b; Moorrees and Reed 1964).

Essentially, Mahalanobis distance is a multivariate form of a univariate statistic that generates a distance measure from a comparison of differences in the means relative to the variance. The univariate form is

$$d^2_{ij} = \frac{\left(\bar{x}_i - \bar{x}_j\right)^2}{\sigma^2}$$

where $\bar{x}_i$ is the mean of the trait in population *i*, $\bar{x}_j$ is the mean of the trait in population *j*, and σ^2 is the variance of the trait. Thus, the multivariate form of this equation is

$$D^2_{ij} = \left(x_i - x_j\right)' V^{-1} \left(x_i - x_j\right)$$

where x_i is a vector of *k* trait means for sample *i*, x_j is a vector of *k* trait means for sample *j*, and V^{-1} is the inverse of the pooled within-group covariance matrix for the *k* traits. One of the

assumptions of Mahalanobis distance is that the within-group covariance matrices for each of the samples compared are approximately equal. I tested the significance of the inter-site D^2 following the methodology of Defrise-Gussenhoven (1967) as recommended by Powell and Neves (1999), where D^2 values greater than $\sqrt{2t-1}$ are significant, with t = number of variables in the analysis.

R Matrix

Both PCA and Mahalanobis distance are model-free approaches to biological distance that do not incorporate population or genetic parameters (Relethford and Lees 1982). As an alternative to these approaches, I used Harpending and Ward's (1982) **R** matrix model. As discussed in Chapter IV, the **R** matrix model compares the heterozygosity of a population to the heterozygosity of the total region. When the observed heterozygosity is greater than the expected heterozygosity, extralocal gene flow occurred, increasing allelic diversity.

As derived by Harpending and Ward (1982) and reviewed in Relethford and Blangero (1990), the formula for expected heterozygosity [$E(H_i)$] of population *i* under a multi-locus, two-allele system is

$$E(H_i) = H_t(1 - r_{ii})$$

where H_t is the heterozygosity of the total region and r_{ii} is the genetic distance between population *i* and the regional centroid. Total region heterozygosity is calculated as

$$H_t = \frac{\sum 2\bar{p}_k \bar{q}_k}{n}$$

where $\bar{p}_k$ and $\bar{q}_k$ are the weighted mean allele frequencies for locus *k*, with summation over a total of *n* loci. Allele frequencies are weighted by the census size (not sample size) of population

i relative to the total census size for all populations. The elements of the **R** matrix for populations *i* and *j* are calculated for any given allele as

$$r_{ij} = \frac{(p_i - \bar{p})(p_j - \bar{p})}{\bar{p}(1 - \bar{p})}$$

The **R** matrix is then averaged for all alleles. The genetic distance of a population to the regional centroid (*rii*) is the diagonal of the **R** matrix. The observed heterozygosity (H_i) for a population is calculated as

$$H_i = \frac{\sum 2 p_{ik} q_{ik}}{n}.$$

Thus, greater than average external gene flow is demonstrated when $H_i > E(H_i)$ and less than average extralocal gene flow is indicated when $H_i < E(H_i)$.

The **R** matrix model was originally designed to be used with genetic systems. However, Relethford and Blangero (1990) have since provided an adaptation of the Harpending and Ward (Harpending and Ward 1982) model for quantitative traits as

$$E[v_i] = \frac{\bar{v}_w (1 - r_{ii})}{1 - F_{ST}}.$$

In this approach, a phenotype, as opposed to a genotype is measured. Nonetheless, for phenotypes under strong genetic control, the same principles of population dynamics hold as those when genotypes are considered. In this model, the expected average phenotypic variance of all measured traits of population *i* is a function of the pooled average within-group phenotypic variation for all measured traits of all of the populations ($\bar{v}_w$), the genetic distance of the population to the combined population centroid (r_{ii}), and the average genetic distance over all the populations (F_{ST}). From the original data, a *g* by *t* matrix **Δ** is formed, where the elements of **Δ** are the deviations of group means from the total means for each trait *t* in population *g*. The

means used to derive the elements of **Δ** are weighted by census population size. Using **Δ**, a codivergence matrix **C** can be calculated as

$$\mathbf{C} = \mathbf{\Delta G}^{-1}\mathbf{\Delta}'$$

where **Δ′** is the transposition of matrix **Δ** and $\mathbf{G}^{-1}$ is the inverse of the additive genetic variance-covariance matrix **G**. Here $\mathbf{G} = h^2\mathbf{P}$, where h^2 is an estimate of trait heritability and **P** is the phenotypic variance-covariance matrix. For this study, I selected a heritability estimate of 0.55 because this value has been successfully used in previous **R** matrix analyses using dental metric data (Stojanowski 2004) and it is an average of the range of heritability estimates of teeth based on family studies (Kieser 1990; Kolakowski and Bailit 1981; Scott and Turner 1997; Townsend and Brown 1978). It is relevant to note that heritability values of anthropometric traits have been found to vary little across human populations (Devor, et al. 1985; Konigsberg and Ousley 1995). In particular, the variability in heritability is expected to be particularly small in this study where all of the samples come from a limited time span, in a relatively circumscribed region with a similar environment, and from a similar ancestral background.

From the codivergence matrix (**C**), F_{ST}—a measure of among-group variance (Wright 1951)—can be calculated as

$$F_{ST} = \frac{\sum_{i=1}^{g} w_i \mathbf{C}_{ii}}{\left(2t + \sum_{i=1}^{g} w_i \mathbf{C}_{ii}\right)}$$

where g and t are as defined above and w_i is the sample weight. When the effective population size is known, sample weight is calculated as

$$w_i = \frac{N_i}{\sum_{j=1}^{g} N_j}$$

here N_j is the effective size of population j. For this study, sample weights are derived from census population sizes. Low values of F_{ST} are found when there is limited among-group genetic variation relative to total variation. From the **C** matrix and total group F_{ST} , the **R** matrix can be computed as

$$\mathbf{R} = \frac{\mathbf{C}(1 - F_{ST})}{2t}.$$

As noted above, the diagonals of the **R** matrix correspond to the genetic distance between each of the populations and the regional centroid. Thus, genetic distances can be derived from the **R** matrix as $d_{ij} = r_{ii} + r_{jj} - 2r_{ij}$ (Harpending and Jenkins 1973). Distances were corrected for sampling error by subtracting $1/2n_i$ from the r_{ii} values, where n_i is the sample size of group i (Relethford 1991). Following Relethford et al. (1997), the variance of F_{ST} can be calculated as

$$\mathrm{var}(F_{ST}) = \left(2/t\right)(1 - F_{ST})\left(\sum \frac{w_i^2 c_{ii}}{n_i}\right)$$

with all variables as defined previously. All **R** matrix calculations were performed with RMET 5.0, authored by John Relethford (Relethford, et al. 1997).

RESULTS

Table 7.6 contains summary data for Classic period dental metrics. The data presented in Table 7.6 represent the original tooth measurements—before imputation or Q-mode transformation. Overall, it is difficult to detect any discernible patterns in the dental metric means and standard deviations due to the shear size of the table. Nonetheless, a few patterns can be observed. First, there does not appear to be any consistent geographic pattern in which sites from the same archaeological zone exhibit similar dental dimensions. Notable exceptions are the

Table 7.6. Sample size, mean, and standard deviation for dental metric traits by site.

SITE	UI1MD			UI1BL			UI2MD			UI2BL		
	N	Mean	s.d.	N	Mean	s.d.	N	Mean	s.d.	N	Mean	s.d.
CENTRAL ZONE												
Tikal	58	8.938	0.556	80	7.381	0.530	61	7.308	0.597	82	6.467	0.652
Tikal: Caches & Pr. Dep.	14	8.924	0.452	12	7.606	0.284	10	7.396	0.906	8	6.510	0.723
Uaxactun	4	8.973	0.849	4	7.295	0.874	2	6.880	0.891	3	6.110	1.034
Calakmul	6	9.095	0.506	18	7.477	0.544	15	7.261	0.549	15	6.451	0.604
USUMACINTA ZONE												
Piedras Negras	31	8.800	0.532	39	7.234	.434	31	7.166	0.633	31	6.357	0.409
PASIÓN ZONE												
Altar de Sacrificios	12	8.719	0.311	18	7.410	.464	17	7.315	0.455	24	6.578	0.449
Seibal	8	8.841	0.569	17	7.210	.334	11	7.034	0.733	16	6.240	0.589
Dos Pilas	7	8.633	0.541	24	7.149	.345	11	7.235	0.562	23	6.275	0.582
Aguateca	4	8.740	0.242	6	7.251	.483	6	7.095	0.680	7	6.366	0.402
Tamarindito	3	8.830	0.756	7	7.216	.326	3	7.110	0.845	6	6.483	0.554
Itzán	2	9.005	0.785	3	6.907	.163	2	6.920	0.127	4	6.418	0.353
BELIZE ZONE												
Altun Ha	29	8.758	0.538	39	7.472	.611	29	7.181	0.692	28	6.472	0.746
Barton Ramie	15	8.661	0.583	21	7.256	.516	14	7.306	0.468	18	6.462	0.554
Baking Pot	2	8.750	0.764	4	7.280	.338	3	7.300	0.848	6	6.370	0.721
Colha	7	8.619	0.346	18	7.372	.589	4	7.118	0.049	12	6.528	0.577
SOUTHWESTERN ZONE												
Copan	7	8.591	0.420	18	7.126	.345	9	6.998	0.909	10	6.258	0.762
HIGHLANDS ZONE												
Kaminaljuyu	8	9.144	0.642	3	7.483	.522	9	7.314	0.472	5	6.190	0.563
PACIFIC COAST ZONE												
Balberta	1	8.420	---	2	6.865	.304	1	6.650	---	2	6.550	0.113
Montana Complex	0	---	---	7	7.171	.276	5	7.610	0.905	8	6.290	0.500
COMBINED SAMPLE	218	8.832	.532	340	7.341	.494	243	7.235	0.625	308	6.418	0.595

Table 7.6. Continued.

SITE	UCMD			UCBL			UP3MD			UP3BL		
	N	Mean	s.d.	N	Mean	s.d.	N	Mean	s.d.	N	Mean	s.d.
CENTRAL ZONE												
Tikal	109	8.373	0.464	106	8.664	0.609	104	7.558	0.448	101	9.518	0.601
Tikal: Caches & Pr. Dep.	14	8.412	0.479	10	8.692	0.407	17	7.674	0.380	17	9.565	0.424
Uaxactun	6	8.067	0.279	6	8.318	0.682	6	7.343	0.672	6	9.152	0.780
Calakmul	23	8.282	0.380	22	8.630	0.671	25	7.516	0.434	25	9.383	0.766
USUMACINTA ZONE												
Piedras Negras	55	8.194	0.431	58	8.350	0.586	48	7.520	0.432	47	9.498	0.627
PASIÓN ZONE												
Altar de Sacrificios	24	8.166	0.482	26	8.509	0.600	23	7.368	0.466	29	9.422	0.515
Seibal	17	8.415	0.537	17	8.745	0.625	20	7.485	0.592	21	9.585	0.770
Dos Pilas	32	8.262	0.496	30	8.597	0.606	35	7.472	0.506	35	9.465	0.634
Aguateca	7	8.089	0.260	7	8.634	0.693	10	7.438	0.375	10	9.456	0.470
Tamarindito	6	7.943	0.615	6	8.213	0.840	7	7.537	0.464	7	10.037	0.667
Itzán	4	8.013	0.430	5	8.196	0.464	4	7.240	0.355	4	9.178	0.555
BELIZE ZONE												
Altun Ha	45	8.191	0.439	54	8.727	0.658	40	7.650	0.561	43	9.677	0.683
Barton Ramie	19	8.357	0.551	21	8.678	0.674	16	7.348	0.564	21	9.570	0.840
Baking Pot	5	8.254	0.344	9	8.641	0.897	7	7.419	0.467	10	9.283	0.975
Colha	11	8.183	0.387	18	8.373	0.900	13	7.312	0.370	13	9.457	0.629
SOUTHWESTERN ZONE												
Copan	15	8.049	0.376	19	8.589	0.573	24	7.510	0.491	21	9.494	0.506
HIGHLANDS ZONE												
Kaminaljuyu	17	8.507	0.384	9	8.702	0.690	14	7.530	0.513	13	9.545	0.575
PACIFIC COAST ZONE												
Balberta	3	8.083	0.601	4	8.055	0.299	2	7.395	0.742	3	9.173	0.397
Montana Complex	4	8.273	0.550	7	8.281	0.504	6	7.425	0.492	6	9.340	0.532
COMBINED SAMPLE	416	8.272	0.461	434	8.575	0.644	421	7.510	0.478	432	9.507	0.641

Table 7.6. Continued.

SITE	UP4MD			UP4BL			UM1MD			UM1BL		
	N	Mean	s.d.	N	Mean	s.d.	N	Mean	s.d.	N	Mean	s.d.
CENTRAL ZONE												
Tikal	103	7.200	0.493	104	9.395	0.616	112	11.095	0.620	110	12.005	0.580
Tikal: Caches & Pr. Dep.	21	7.322	0.452	20	9.402	0.593	13	11.085	0.515	15	11.894	0.362
Uaxactun	6	7.078	0.576	6	9.208	0.922	5	10.642	0.293	5	11.524	0.408
Calakmul	20	7.147	0.305	21	9.209	0.696	25	10.774	0.519	24	11.828	0.596
USUMACINTA ZONE												
Piedras Negras	44	7.193	0.448	46	9.281	0.538	45	10.906	0.621	41	11.761	0.604
PASIÓN ZONE												
Altar de Sacrificios	19	7.111	0.356	30	9.246	0.604	22	10.970	0.603	28	11.895	0.657
Seibal	18	7.154	0.498	23	9.596	0.799	19	11.051	0.475	20	12.058	0.427
Dos Pilas	33	7.288	0.470	33	9.362	0.693	36	10.891	0.671	30	11.915	0.576
Aguateca	9	7.090	0.407	9	9.351	0.288	8	10.691	0.467	7	11.817	0.448
Tamarindito	6	7.403	0.540	7	9.784	0.867	4	10.695	0.527	5	11.774	0.561
Itzán	4	6.830	0.416	5	9.110	0.796	3	10.837	0.476	3	11.493	0.210
BELIZE ZONE												
Altun Ha	36	7.293	0.515	41	9.448	0.741	48	11.068	0.692	52	12.013	0.681
Barton Ramie	16	7.013	0.467	23	9.295	0.669	11	10.649	0.974	14	11.739	0.689
Baking Pot	5	7.386	0.382	8	9.340	0.975	4	10.698	0.580	6	11.452	0.772
Colha	7	6.873	0.510	11	9.534	0.663	10	10.991	0.495	11	11.906	0.513
SOUTHWESTERN ZONE												
Copan	17	7.109	0.435	22	9.398	0.536	22	10.910	0.545	25	12.062	0.540
HIGHLANDS ZONE												
Kaminaljuyu	15	7.471	0.484	12	9.278	0.635	16	11.022	0.604	15	11.860	0.531
PACIFIC COAST ZONE												
Balberta	3	6.720	0.419	3	8.803	0.230	2	10.485	0.064	1	10.830	----
Montana Complex	5	7.014	0.299	5	9.016	0.680	9	10.993	0.485	9	11.589	0.652
COMBINED SAMPLE	387	7.197	0.470	429	9.362	0.653	414	10.970	0.615	421	11.909	0.593

Table 7.6. Continued.

SITE	UM2MD			UM2BL			LI1MD			LI1BL		
	N	Mean	s.d.	N	Mean	s.d.	N	Mean	s.d.	N	Mean	s.d.
CENTRAL ZONE												
Tikal	106	10.087	0.640	103	11.942	0.705	40	5.772	0.414	42	5.774	0.396
Tikal: Caches & Pr. Dep.	16	10.048	0.816	15	11.730	0.705	5	5.518	0.400	6	5.848	0.296
Uaxactun	5	9.268	0.636	5	11.066	0.792	2	5.745	0.375	1	5.920	---
Calakmul	16	9.681	0.541	13	11.926	0.969	15	5.597	0.326	12	5.769	0.347
USUMACINTA ZONE												
Piedras Negras	44	10.079	0.744	41	11.417	0.904	30	5.669	0.325	22	5.630	0.357
PASIÓN ZONE												
Altar de Sacrificios	25	9.875	0.597	27	11.729	0.718	7	5.593	0.233	15	5.926	0.372
Seibal	20	9.919	0.540	21	12.184	0.595	4	5.350	0.203	13	5.729	0.477
Dos Pilas	38	9.917	0.684	32	11.958	0.716	9	5.576	0.322	17	5.688	0.323
Aguateca	9	9.998	0.548	7	11.570	0.283	2	5.640	0.057	5	5.630	0.320
Tamarindito	7	10.361	0.683	6	11.948	0.630	4	5.735	0.488	4	5.528	0.413
Itzán	4	9.963	1.075	4	11.753	0.871	2	5.995	0.332	2	5.640	0.212
BELIZE ZONE												
Altun Ha	48	9.824	0.690	42	11.722	0.672	22	5.596	0.391	26	5.775	0.323
Barton Ramie	13	9.758	0.978	12	11.993	1.232	7	5.520	0.327	12	5.629	0.332
Baking Pot	3	10.203	0.782	6	11.980	0.979	2	5.445	0.078	1	5.670	---
Colha	10	9.739	0.686	11	11.565	0.655	6	5.722	0.395	9	5.846	0.296
SOUTHWESTERN ZONE												
Copan	20	9.934	0.397	20	11.670	0.409	6	5.698	0.187	7	5.733	0.414
HIGHLANDS ZONE												
Kaminaljuyu	15	10.082	0.611	14	11.669	0.648	7	5.660	0.484	2	6.050	0.410
PACIFIC COAST ZONE												
Balberta	2	8.825	0.346	3	10.807	1.022	0	---	---	0	---	---
Montana Complex	7	9.829	0.586	6	11.177	0.779	2	5.930	0.028	3	5.517	0.182
COMBINED SAMPLE	408	9.956	0.674	388	11.781	0.763	172	5.660	0.361	199	5.743	0.361

Table 7.6. Continued.

SITE	LI2MD			LI2BL			LCMD			LCBL		
	N	Mean	s.d.	N	Mean	s.d.	N	Mean	s.d.	N	Mean	s.d.
CENTRAL ZONE												
Tikal	62	6.377	0.440	67	6.223	0.431	113	7.266	0.461	80	7.818	0.554
Tikal: Caches & Pr. Dep.	8	6.393	0.348	3	6.320	0.332	13	7.367	0.527	8	8.283	0.471
Uaxactun	2	6.420	0.269	0	---		3	7.600	0.663	3	8.493	0.827
Calakmul	17	6.383	0.405	12	6.258	0.321	25	7.233	0.440	15	8.003	0.527
USUMACINTA ZONE												
Piedras Negras	43	6.400	0.360	31	6.091	0.306	48	7.103	0.417	37	7.577	0.419
PASIÓN ZONE												
Altar de Sacrificios	15	6.302	0.346	24	6.159	0.385	28	7.185	0.519	22	7.764	0.753
Seibal	5	6.224	0.271	15	6.367	0.293	9	7.184	0.364	8	7.643	0.633
Dos Pilas	20	6.442	0.437	23	6.103	0.364	32	7.258	0.381	27	7.643	0.517
Aguateca	4	6.343	0.362	5	6.028	0.337	11	7.093	0.204	9	7.482	0.406
Tamarindito	5	6.416	0.250	6	5.832	0.264	8	7.375	0.423	5	7.814	0.708
Itzán	4	6.390	0.472	6	6.048	0.212	5	7.256	0.225	4	7.680	0.446
BELIZE ZONE												
Altun Ha	27	6.322	0.380	26	6.388	0.380	34	7.158	0.349	25	7.784	0.540
Barton Ramie	12	6.278	0.428	15	6.204	0.468	12	7.278	0.494	10	8.085	0.856
Baking Pot	3	5.820	0.128	3	6.030	0.469	4	7.070	0.224	5	7.642	0.706
Colha	9	6.200	0.392	11	6.103	0.445	15	7.019	0.292	9	7.828	0.524
SOUTHWESTERN ZONE												
Copan	7	6.411	0.437	11	6.283	0.386	13	7.425	0.321	5	7.928	0.339
HIGHLANDS ZONE												
Kaminaljuyu	8	6.304	0.274	3	6.120	0.424	14	7.197	0.245	6	7.790	0.575
PACIFIC COAST ZONE												
Balberta	1	5.730	---	1	5.650	---	3	7.353	0.391	2	7.610	1.499
Montana Complex	6	6.327	0.244	5	6.100	0.199	5	7.132	0.423	6	8.122	1.291
COMBINED SAMPLE	258	6.352	0.389	267	6.191	0.387	395	7.221	0.422	286	7.788	0.600

Table 7.6. Continued.

SITE	LP3MD			LP3BL			LP4MD			LP4BL		
	N	Mean	s.d.	N	Mean	s.d.	N	Mean	s.d.	N	Mean	s.d.
CENTRAL ZONE												
Tikal	117	7.232	0.538	100	7.949	0.534	111	7.428	0.506	105	8.461	0.580
Tikal: Caches & Pr. Dep.	11	7.258	0.436	8	7.876	0.596	21	7.617	0.560	23	8.506	0.591
Uaxactun	3	7.550	0.632	2	7.865	0.431	3	7.497	1.117	3	8.743	0.586
Calakmul	28	7.099	0.380	28	7.960	0.477	26	7.310	0.473	27	8.366	0.532
USUMACINTA ZONE												
Piedras Negras	51	7.182	0.428	46	7.781	0.505	53	7.450	0.440	51	8.306	0.492
PASIÓN ZONE												
Altar de Sacrificios	30	6.963	0.638	25	7.948	0.611	22	7.285	0.522	26	8.296	0.582
Seibal	18	7.116	0.450	18	8.140	0.449	23	7.320	0.647	22	8.461	0.657
Dos Pilas	39	7.145	0.486	33	7.953	0.484	41	7.405	0.576	36	8.451	0.565
Aguateca	11	7.237	0.494	11	8.168	0.565	10	7.312	0.353	11	8.348	0.612
Tamarindito	7	7.290	0.459	6	8.092	0.551	8	7.475	0.373	8	8.414	0.559
Itzán	3	6.933	0.549	4	7.940	0.504	4	7.150	0.312	4	8.143	0.355
BELIZE ZONE												
Altun Ha	38	7.179	0.496	41	8.013	0.564	48	7.432	0.431	48	8.389	0.566
Barton Ramie	20	7.095	0.633	21	8.031	0.682	19	7.220	0.587	24	8.172	0.616
Baking Pot	3	7.350	0.650	4	7.553	0.577	2	7.485	0.078	6	8.020	0.585
Colha	14	6.906	0.304	13	7.878	0.534	12	7.293	0.415	10	8.362	0.496
SOUTHWESTERN ZONE												
Copan	24	7.147	0.338	20	8.039	0.390	29	7.478	0.381	28	8.461	0.502
HIGHLANDS ZONE												
Kaminaljuyu	16	7.125	0.392	10	7.952	0.568	13	7.497	0.626	13	8.293	0.569
PACIFIC COAST ZONE												
Balberta	1	6.640	---	1	7.150	---	3	7.453	0.750	3	8.313	0.562
Montana Complex	4	7.048	0.606	3	7.990	0.392	5	7.204	0.279	6	8.132	0.459
COMBINED SAMPLE	438	7.156	0.495	394	7.953	0.531	453	7.406	0.502	454	8.384	0.562

Table 7.6. Continued.

SITE	LM1MD			LM1BL			LM2MD			LM2BL		
	N	Mean	s.d.	N	Mean	s.d.	N	Mean	s.d.	N	Mean	s.d.
CENTRAL ZONE												
Tikal	124	11.958	0.595	126	11.001	0.558	114	11.455	0.707	112	10.461	0.554
Tikal: Caches & Pr. Dep.	25	12.114	0.639	25	11.174	0.505	20	11.738	0.672	22	10.583	0.591
Uaxactun	5	11.784	0.322	5	10.792	0.528	4	10.820	0.304	4	9.880	0.777
Calakmul	22	11.755	0.452	17	10.948	0.556	25	11.308	0.639	22	10.491	0.560
USUMACINTA ZONE												
Piedras Negras	51	11.732	0.600	49	10.747	0.582	45	11.259	0.689	41	10.332	0.587
PASIÓN ZONE												
Altar de Sacrificios	27	11.765	0.560	30	10.781	0.508	19	11.117	0.654	25	10.411	0.520
Seibal	20	11.809	0.485	21	10.758	0.389	18	11.553	0.983	18	10.597	0.760
Dos Pilas	36	11.691	0.589	31	10.955	0.525	34	11.376	0.726	33	10.540	0.535
Aguateca	7	11.867	0.313	7	10.644	0.164	5	10.862	0.504	5	10.364	0.299
Tamarindito	6	11.927	0.434	6	10.923	0.581	6	11.275	0.515	4	10.413	0.530
Itzán	4	12.005	0.700	4	11.065	0.723	5	11.285	0.769	4	10.360	0.488
BELIZE ZONE												
Altun Ha	52	11.926	0.459	57	10.890	0.504	48	11.393	0.593	44	10.365	0.552
Barton Ramie	14	11.594	0.888	19	10.897	0.688	16	11.163	0.879	17	10.417	0.800
Baking Pot	4	11.513	0.867	4	10.923	0.944	4	11.483	0.869	4	10.498	1.028
Colha	13	11.855	0.465	13	11.094	0.415	11	11.270	0.381	11	10.419	0.505
SOUTHWESTERN ZONE												
Copan	24	12.000	0.511	24	11.040	0.458	25	11.329	0.546	26	10.519	0.470
HIGHLANDS ZONE												
Kaminaljuyu	11	11.655	0.526	9	10.918	0.480	14	11.518	0.737	14	10.534	0.788
PACIFIC COAST ZONE												
Balberta	4	12.443	0.779	2	11.050	1.131	2	10.335	0.474	2	9.745	0.417
Montana Complex	8	11.754	0.301	8	10.735	0.395	6	11.022	0.692	6	10.217	0.672
COMBINED SAMPLE	457	11.863	0.574	457	10.924	0.540	420	11.364	0.696	414	10.444	0.584

sites from the Pacific Coast which, on average, appear to exhibit smaller teeth than the other sites in the sample. However, when the standard deviations are considered, there does not seem to be any apparent trend for greater or lesser variability at any of the sites, especially among those with relatively large sample sizes ($n > 20$). Further univariate and multivariate analyses can better explore the differences in dental metrics between Maya sites.

Temporal Trends

In his analysis of dental metric variability in Belize, Wrobel (2003) detected a general decrease in tooth size from Preclassic to Historic times. My study is limited to the Classic period and the majority of the sample dates to the Late and Terminal Classic periods, thus there was little time for natural selection to create a substantial trend in tooth size among the samples. Nonetheless, I examined the dental metric data for a chronological trend at Tikal, the largest sample in this study (N=234, excluding caches and problematic deposits). For this analysis, I included data from the Preclassic period to increase the temporal range, and I pooled data from the Middle Preclassic and Late Preclassic periods due to their small sample sizes. Preclassic data is not considered in any other aspect of this work.

I calculated crown areas by multiplying the mesiodistal length by the buccolingual breadth for each case. I determined mean crown areas for each tooth; these are plotted in Figures 7.1 and 7.2. These graphs indicate there is no apparent chronological trend in dental size at Tikal. I verified the lack of chronological trend through linear regression analysis. I regressed crown tooth area against the median date of each time period and considered each tooth in a separate regression analysis. None of the 16 analyses performed had resulting *F*-ratios that approached significance ($0.283 < p < 0.938$). Although there is clearly some variability in

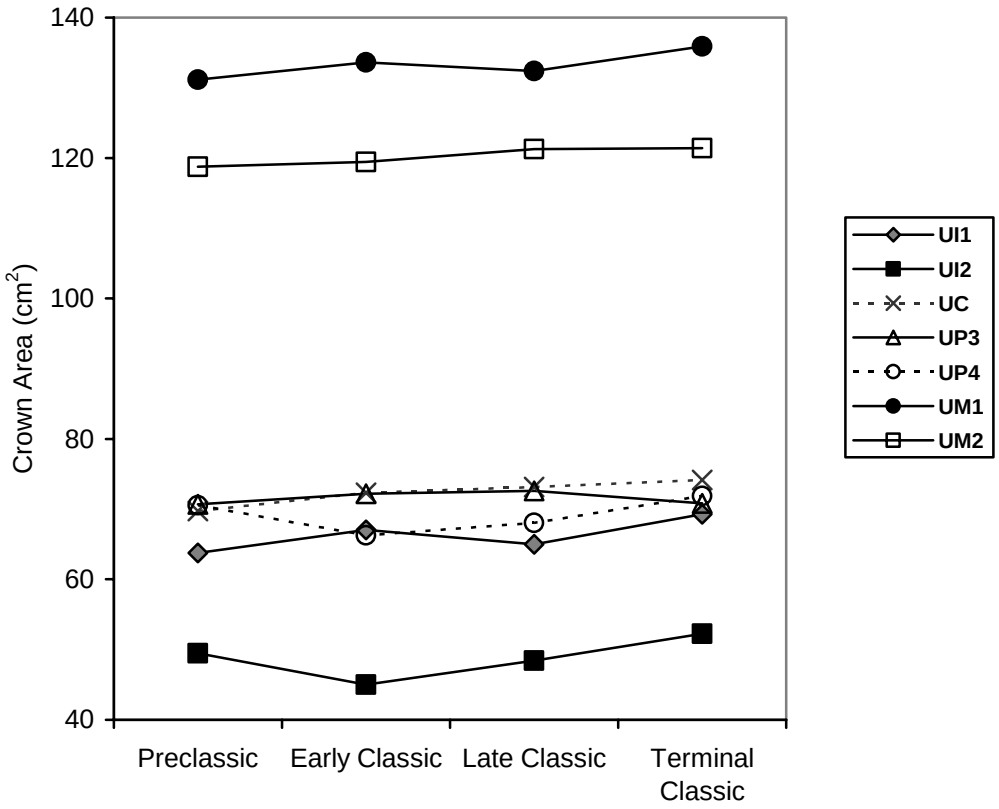

Figure 7.1. Chronological differences in maxillary crown area at Tikal, Guatemala.

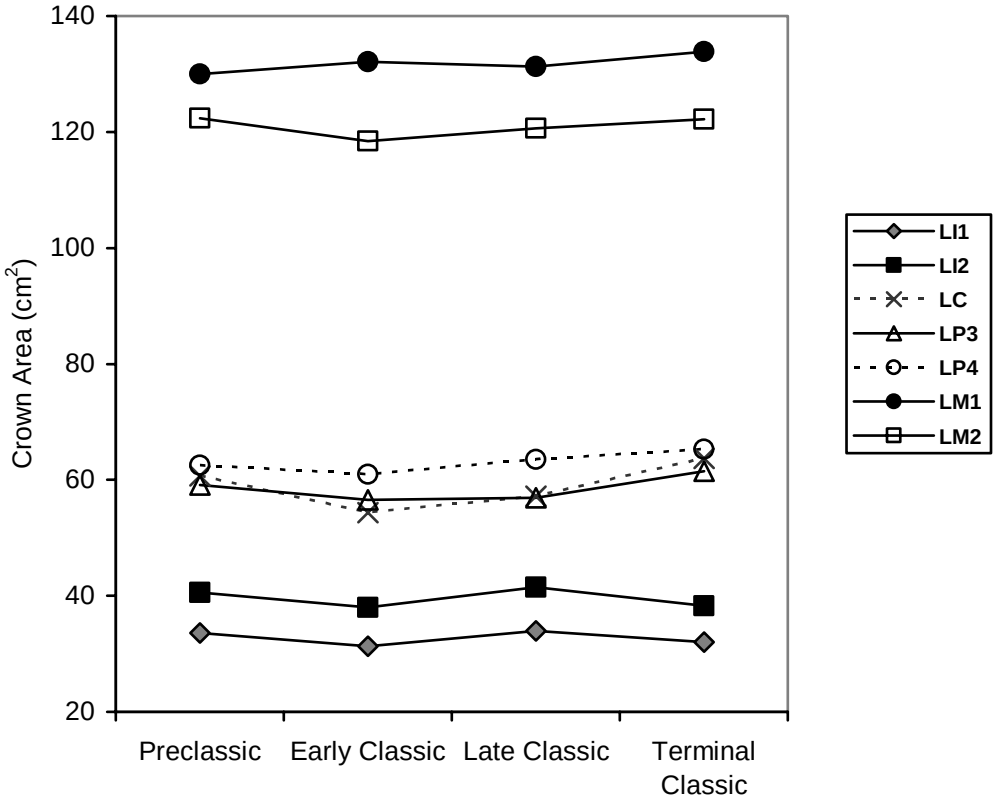

Figure 7.2. Chronological differences in mandibular crown area at Tikal, Guatemala.

crown area by time period, the apparent randomness of these differences indicates that historical processes such as gene flow or genetic drift are responsible for them, not directional selection.

Wrobel (2003) has documented a chronological trend for decreased tooth size amongst the northern Belize Maya. A similar trend has been noted for other parts of the world, which is interpreted to be the result of changes in food processing techniques and an increase in agricultural reliance (Brace, et al. 1991; Calcagno 1989; Calcagno and Gibson 1988; Christensen 1998c). No such trend is found here. In fact, if any chronological change occurred, it was an *increase* in crown size from the Late to Terminal Classic periods at Tikal. I performed an ANOVA to determine if any of the teeth possessed a statistically significant change in crown area over time at Tikal. The results of this analysis are presented in Table 7.7. None of the analyses were significant, indicating no statistically significant temporal change in crown area at Tikal. Only one tooth, LC, has a change in crown area that approaches significance ($p = 0.053$) and this is due to an increase in crown size during the Classic period. Further, this may simply be the result of familywise error.

This intra-site analysis of temporal trends in tooth size is in conflict with the results obtained in Wrobel's study. Although it is possible that dental reduction occurred in Belize, but not at Tikal, an equally plausible possibility is that the trend observed in Wrobel's study is the product of combining samples from a number of different sites. In Wrobel's study, different time periods are more heavily represented at certain sites, thus what Wrobel might be interpreting as a chronological trend may in fact be due to population differences in dental metrics.

Table 7.7. ANOVA of crown area by archaeological period at Tikal.

	Mean Crown Area					
	Preclassic	**Early Classic**	**Late Classic**	**Terminal Classic**	***F***	***p***
UI1	63.76	67.03	64.97	69.28	0.421	0.738
UI2	49.49	45.04	48.44	52.29	1.469	0.234
UC	69.74	72.35	73.17	74.15	0.356	0.785
UP3	70.67	72.21	72.59	70.82	0.193	0.901
UP4	70.55	66.27	68.04	71.87	0.936	0.426
UM1	131.17	133.60	132.38	135.89	0.226	0.878
UM2	118.74	119.44	121.27	121.41	0.216	0.885
LI1	33.59	31.25	33.95	32.03	10.873	0.596
LI2	40.56	37.99	41.47	38.25	2.172	0.108
LC	60.66	54.36	57.14	63.74	2.689	0.053
LP3	59.10	56.53	56.90	61.46	0.908	0.440
LP4	62.46	60.96	63.52	65.23	0.832	0.479
LM1	130.12	132.12	131.24	133.89	0.184	0.907
LM2	122.36	118.39	120.59	122.15	0.401	0.753

Analysis of Variance

In order to better determine whether any differences exist in the mean and variability of dental measurements between Classic period sites, a series of simple univariate statistics were performed. ANOVA was used to determine whether any of the measurements exhibited statistically significant differences in their means across the sites. I only included sites in the ANOVA that are also used in later biological distance analyses.

Table 7.8 shows that no measurement means are significantly different between sites. However, four measurements, all polar teeth, approach significance: UI1BL ($p = 0.051$). UCMD ($p = 0.052$), UM1MD ($p = 0.051$), LM1MD ($p = 0.070$). These data point towards a general homogeneity in dental dimensions across the Maya area.Levene's test indicates that the variance of LCMD and LP3MD was statistically different between some sites. Taken together, the results of ANOVA and Levene's test demonstrate only subtle variability in dental metric means and intra-site variability in the Maya area during the Classic period.

Using the imputed dataset, I performed a MANOVA. Using Wilk's λ test statistic, I obtained the following results: Wilk's $\lambda = 0.723$; $F = 1.146$; degrees of freedom = 88, 1989.806; $p = .171$. These results indicate that there is no statistically significant difference in measurement means across the sites when all of the measurements are considered simultaneously.

Although pointing towards homogeneity in dental dimensions in the Maya area, a lack of statistically significant differences in measurement means and variances does not preclude further multivariate analysis. Regional homogeneity in both dental metrics (Powell 1995) and cranial metrics (Powell and Neves 1999; Relethford and Harpending 1994; Relethford and Harpending 1995) have been observed in other studies where significant multivariate differences

Table 7.8. ANOVA of between-site differences in mean measurements.

Trait	Levene's (*p*)	*F* (*p*)
UI1MD	1.196 (0.291)	1.323 (0.213)
UI1BL	1.432 (0.157)	1.810 (0.051)
UI2MD	1.511 (0.128)	0.497 (0.904)
UCMD	0.726 (0.714)	1.521 (0.121)
UCBL	1.577 (0.103)	1.801 (0.052)
UP3BL	1.268 (0.241)	0.411 (0.951)
UP4BL	0.660 (0.776)	1.165 (0.310)
UM1MD	1.629 (0.088)	1.504 (0.127)
UM1BL	1.111 (0.351)	1.806 (0.051)
UM2MD	1.204 (0.282)	1.710 (0.069)
LI1MD	1.207 (0.286)	1.094 (0.370)
LI1BL	0.479 (0.915)	1.185 (0.300)
LI2BL	0.747 (0.692)	1.374 (0.185)
LCMD	**1.875 (0.041)**[1]	1.269 (0.241)
LP3MD	**2.152 (0.016)**	1.029 (0.419)
LP3BL	1.127 (0.339)	1.210 (0.278)
LP4BL	0.440 (0.938)	0.793 (0.647)
LM1MD	1.665 (0.079)	1.706 (0.070)
LM1BL	0.741 (0.699)	1.308 (0.217)
LM2MD	1.374 (0.182)	1.340 (0.200)
LM2BL	1.639 (0.086)	0.966 (0.477)

[1]Values in bold are significant at the .05 level

were found. Multivariate statistics can often detect inter-sample differences even when univariate approaches fail to do so (Manly 1994).

Principal Components Analysis

Table 7.9 shows the matrix obtained from the Principal Component Analysis (PCA). Three components that explain 67.99% of the variance were extracted. The first component, which explains 35.91% of the variance, is heavily loaded on measurements of the first maxillary and mandibular molars and negatively loaded on LP4BL. The second component, which explains 14.98% of the variance, is positively loaded with measurements of the mandibular molar teeth and negatively loaded with maxillary teeth and mandibular premolar measurements. The third component, which explains 14.80% of the variance, is moderately loaded on the buccolingual measurements and negatively loaded on mesiodistal measurements of both the maxillary and mandibular teeth.

For ease of comparison, the Classic Maya site PCA centroids were plotted in three dimensional space (Figure 7.3). A majority of the sites cluster in the center of the plot, particularly along the second principal component. However, a number of sites also plot away from the other sites: Piedras Negras, Kaminaljuyu, Pacific Coast, Altar de Sacrificios, Barton Ramie, and Altar de Sacrificios. The separation of Kaminaljuyu and the Pacific Coast from the remaining Maya sites is not surprising considering the archaeological differences and geographic distance between these two sites and the remaining sites in the sample.

Mahalanobis Distance

As an alternative to PCA, I performed a Mahalanobis distance analysis. The results of the Mahalanobis distance analysis, based on nine dental measurements, are presented in

Table 7.9. Extracted components from PCA.

	Component 1	Component 2	Component 3
UP3BL	-0.5050	-0.5162	0.3373
UM1MD	0.6992	-0.0683	-0.2607
UM1BL	0.6553	-0.2118	0.4163
LP3MD	-0.4993	-0.3560	-0.6303
LP4BL	-0.6994	-0.1815	0.3292
LM1MD	0.7550	0.0675	-0.3396
LM1BL	0.7056	0.1040	0.3304
LM2.MD	-0.4079	0.6952	-0.3281
LM2.BL	-0.2921	0.7518	0.3943
EIGENVALUE	3.1395	1.5282	1.3764

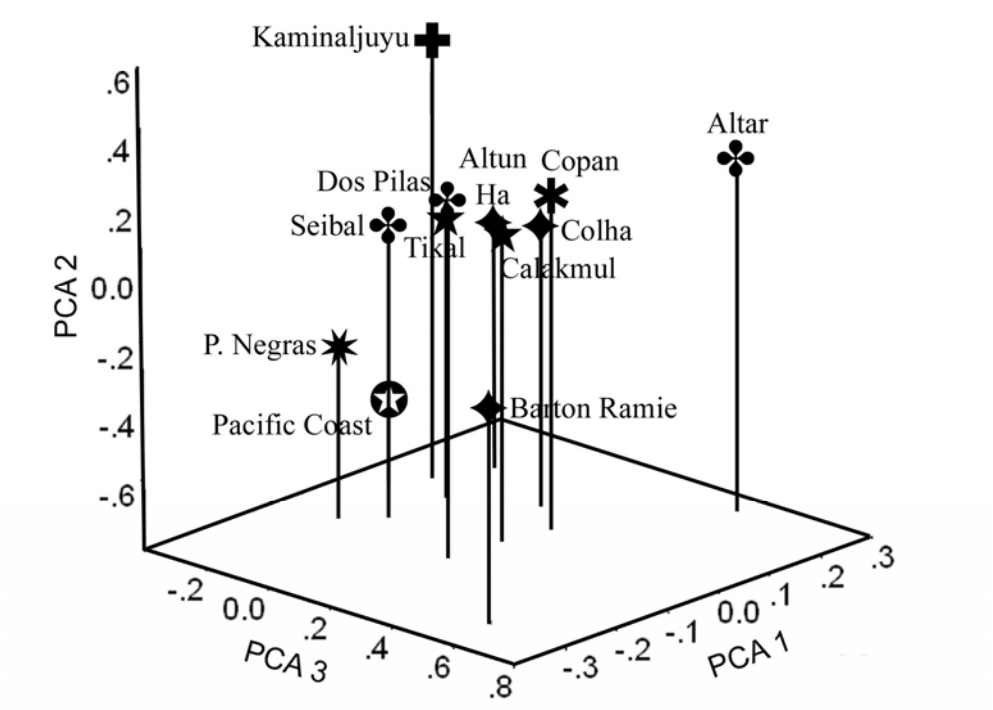

Figure 7.3. Principal components plot of Classic period sites based on dental metric traits.

Table 7.10. Following the methodology of Defrise-Gussenhoven (1967), pairwise distances greater than 4.123 would be significant. However, none of the distances were found to be significant and only the Kaminaljuyu-Pacific Coast comparison approaches statistical significance (4.0669). This underscores the relative homogeneity in dental dimensions in the Maya area that was first identified by ANOVA and MANOVA.

Overall, there is little concordance between Mahalanobis distance and geographic distance in the Maya area. In order to confirm this observation, I performed a Mantel test. The geographic distance matrix used for this comparison is presented in Table 6.8 of the previous chapter. The following results were obtained: $r = .2443$; $r^2 = .0597$; $p = 0.2770$. In a Mantel's test, a statistically significant r^2 indicates a correlation between the two distance matrices. Clearly, the geographic distance matrix is not correlated with the Mahalanobis distance matrix.

In the Mantel test for nonmetric traits (based on the MMD analysis), I did not include the Pacific Coast sample due to its small sample size. Thus, I re-ran the Mantel test for the Mahalanobis distance matrix excluding the Pacific Coast in order to determine whether the addition of this site affected the results. For this test, I obtained $r = 0.1429$ and $r^2 = .0204$, with a significance of $p = .4570$. Not surprisingly, the correlation between geographic distance and biological distance was even further reduced when the geographically outlying Pacific Coast was removed from the analysis.

The Mahalanobis distances were plotted using multidimensional scaling (MDS) in order to better understand the results (Figure 7.4). Generally, the MDS plot is very similar to the three dimensional plot of the first three components of the PCA. In both plots, Kaminaljuyu and the Pacific Coast are major outliers. This suggests an overall separation of lowland Maya sites from these non-lowland sites to the south. Further, these sites show a lack of affinity to one another.

Table 7.10. Mahalanobis distances between Classic period samples.

	Tikal	Calak-mul	Piedras Negras	Altar	Seibal	Dos Pilas	Altun Ha	Barton Ramie	Colha	Copan	KJ
Calakmul	0.3824	---									
Piedras Negras	0.3837	0.7029	---								
Altar	1.0092	1.0623	1.0915	---							
Seibal	0.8787	1.7889	1.0831	1.5656	---						
Dos Pilas	0.6358	0.2284	0.7675	0.9306	1.6289	---					
Altun Ha	0.1955	0.8706	0.4326	0.8579	0.8004	0.9951	---				
Barton Ramie	1.3501	1.1029	1.4285	1.3970	1.2917	1.0017	1.4565	---			
Colha	0.2547	0.1837	0.8720	1.3311	1.6353	0.6918	0.6800	1.2593	---		
Copan	0.5529	0.6705	1.0984	1.1607	1.2817	0.8303	0.9251	1.2715	0.6351	---	
Kaminal-juyu	1.9247	1.5850	1.8053	1.6888	2.3490	1.1803	1.8984	1.8483	1.9888	2.5450	---
Pacific Coast	1.4998	1.6695	0.8520	2.6667	2.6095	1.7349	1.9009	3.3219	2.1170	1.9944	4.0669

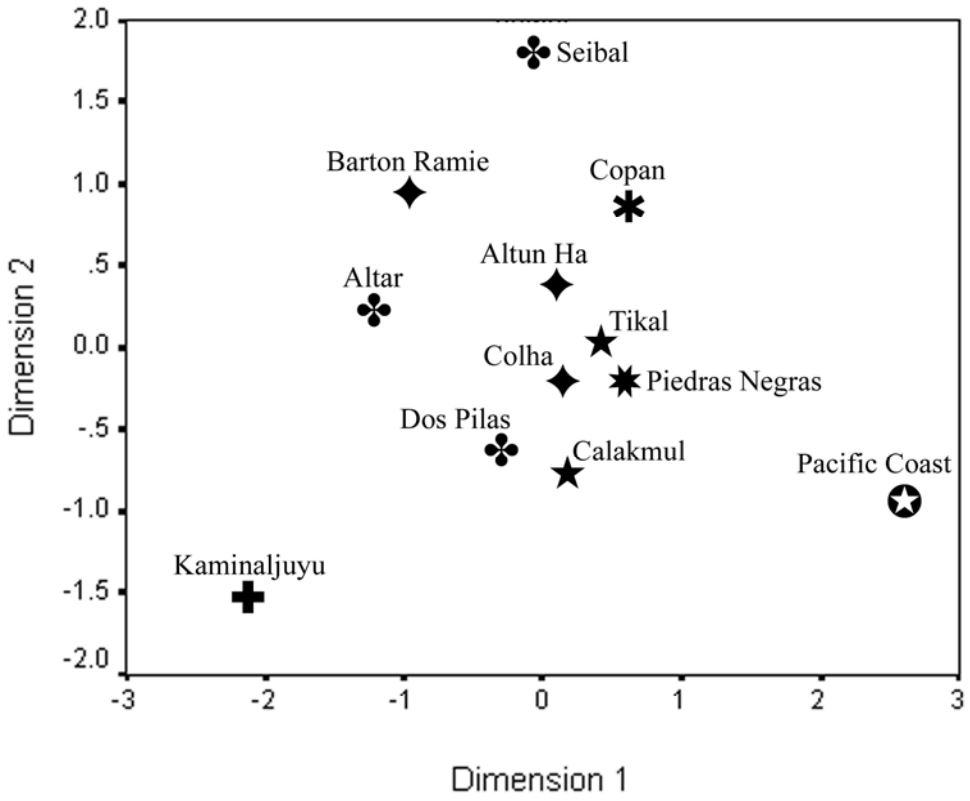

Figure 7.4. Multidimensional scaling plot of Classic period Mahalanobis distances. Archaeological Zones: Central (★), Pasión (✤), Usumacinta (✸), Belize (✦), Southeast (✱), Highlands (✚).

In both the MDS and PCA plot, the majority of other Maya sites form a cluster in the center of the plot. In the PCA plot, Barton Ramie, Piedras Negras, and Altar de Sacrificios are outliers. In the MDS plot, Barton Ramie, Altar de Sacrificios, and Seibal are separated from the main cluster, whereas in the PCA plot Piedras Negras is more isolated than is Seibal. The remaining sites form a cluster in both plots, with generally the same association to one another. Altun Ha, Colha, and Tikal all plot near one another. Dos Pilas and Calakmul are also neighbors, though Dos Pilas is more removed in the PCA plot.

R Matrix

I performed an **R** matrix analysis (Harpending and Ward 1982) following the methodology of Relethford and Blangero (Relethford 1991; Relethford and Blangero 1990; Relethford, et al. 1997). Although I selected a heritability value of 0.55, I also ran the **R** matrix analysis using heritability values between 0.55 and 1.00. None of the permutations produced differing results. Thus, I present all **R** matrix analyses with the original heritability estimate of 0.55. The results of the **R** matrix analysis are bias-corrected for differences in sample size between sites.

Table 7.11 shows the F_{ST} results, which provide a measure of among-group variation in the Maya area. When all of the sites are considered as a single sample, an F_{ST} of 0.0182 is obtained. In comparison to other F_{ST} values obtained from phenotypic analyses of quantitative traits (Jantz and Meadows 1995; Steadman 1998; Stojanowski 2004; Tatarek and Sciulli 2000), 0.0182 is a relatively low value, indicating limited among-group genetic variability in the Maya area. These results underscore earlier observations of dental metric homogeneity in this study. When the Maya lowlands alone are considered—excluding Kaminaljuyu and the Pacific Coast—an even lower F_{ST} of 0.0117 is found. This indicates substantial gene flow between Maya sites

Table 7.11. F_{ST} values for the Maya area.

Grouping	# of Sites	F_{ST}	Standard Error
Central Zone	2	0.0031	0.0051
Pasión Zone	3	0.0181	0.0125
Belize Zone	3	0.0189	0.0141
Maya Lowlands	10	0.0117	0.0054
Total Maya Area	12	0.0182	0.0079

throughout the Classic period, with relatively little genetic drift. Although the standard error for these F_{ST} estimates is high relative to the F_{ST} values, the error range is still well within the limits we would expect for interbreeding populations (Wright 1951).

Since the Central, Pasión, and Belize Zones are represented by multiple sites, I was able to calculate F_{ST} for each of these regions separately. The Central Zone is characterized by a very low F_{ST}, whereas both the Belize and Pasión Zones possess much higher values. The small F_{ST} for the Central Zone is not surprising since it is represented by the colossal sites of Tikal and Calakmul. The lack of differentiation between the two is likely due to their long-term large population size (lack of genetic drift) and, perhaps, a degree of phenotypic continuity across the Central Petén. This would be in contrast to a model that proposes substantial gene flow between Calakmul and Tikal, which is unlikely due to their bitter enmity throughout the Classic period (Martin and Grube 1995, 2000). In order to understand the high F_{ST} values for the Belize and Pasión Zones, I will turn to the results of the Relethford-Blangero analysis (Table 7.12).

In the Relethford-Blangero analysis, negative residuals indicate below average extra-local gene flow, whereas positive values indicate greater than average extra-local gene flow. Table 7.12 shows that the majority of the residual values are small and most are negative, indicating very little foreign gene flow into the populations sampled. However, three sites, Kaminaljuyu, Seibal, and Barton Ramie, possess large, positive residuals. This suggests gene flow into these sites from either a region outside of the Maya area of this analysis, or from sites within the region, but not sampled here.

I re-ran the Relethford-Blangero analyses for each of the archaeological zones that contained more than one site (Central, Pasión, and Belize), excluding all of the sites from outside the respective zone in the analysis (Table 7.13 – Table 7.15). If mating networks were largely restricted to within each zone, the residuals should be negative or near zero. In the Central Zone

Table 7.12. Results of Relethford-Blangero analysis for the total Maya area.

Population	r(ii)	Observed Variance	Expected Variance	Residual
Tikal	0.0065	0.916	1.029	-0.113
Calakmul	0.0000	0.946	1.036	-0.090
Piedras Negras	0.0333	0.998	1.001	-0.003
Altar	0.0674	0.961	0.966	-0.005
Seibal	0.0757	1.498	0.957	0.541
Dos Pilas	0.0100	1.020	1.025	-0.005
Altun Ha	0.0250	0.971	1.010	-0.039
Barton Ramie	0.0810	1.322	0.952	0.371
Colha	0.0000	0.872	1.036	-0.164
Copan	0.0118	0.859	1.024	-0.164
Kaminaljuyu	0.0570	1.486	0.977	0.509
Pacific Coast	0.1399	0.794	0.891	-0.097

Table 7.13. Results of Relethford-Blangero analysis for the Central Zone only.

Population	r(ii)	Observed Variance	Expected Variance	Residual
Tikal	0.0075	0.998	1.010	-0.012
Calakmul	0.0000	1.026	1.018	0.008

Table 7.14. Results of Relethford-Blangero analysis for the Pasión Zone only.

Population	r(ii)	Observed Variance	Expected Variance	Residual
Altar	0.0634	0.842	1.089	-0.247
Seibal	0.0000	1.315	1.163	0.152
Dos Pilas	0.0371	0.940	1.120	-0.179

Table 7.15. Results of Relethford-Blangero analysis for the Belize zone only.

Population	r(ii)	Observed Variance	Expected Variance	Residual
Altun Ha	0.0345	0.946	0.931	0.015
Barton Ramie	0.0393	1.323	0.927	0.396
Colha	0.0000	0.807	0.965	-0.157

(Table 7.13), Tikal and Calakmul each demonstrate near-zero residuals indicating a balance between intra-zonal and extra-zonal gene flow. For the Pasión (Table 7.14) and Belize Zone (Table 7.15), the majority of sites exhibit near zero residuals or negative residuals, indicating moderate to low extra-local gene flow. However, Seibal of the Pasión Zone and Barton Ramie of the Belize Zone exhibit large positive residuals, further highlighting the evidence for substantial genetic deviation for these sites relative to the other sites within their respective zones.

Table 7.16 presents the biological distances obtained from the unscaled **R** matrix analysis. In general, Kaminaljuyu and the Pacific Coast demonstrate the greatest biological distances from the other sites in the sample. The remaining sites show relatively small distances to one another. This pattern is similar to what was seen in the Mahalanobis Distance analysis. I performed a Mantel test between the unscaled **R** matrix genetic distance matrix and the geographic distance matrix (Table 6.8). The results of this analysis indicate a lack of association between genetic distance and geographic distance ($r = 0.1749$; $r^2 = 0.0306$; $p = 0.4370$).

A PCA plot of the first two components of the unscaled **R** matrix is presented in Figure 7.5. The first eigenvector accounts for 47.3% of the variation and the second accounts for 21.5% of the variation for a total of 68.8%. The plot is very similar to those obtained for the other multivariate analyses. In fact, the **R** matrix eigenvector plot is a near replica of the MDS ordination of the Mahalanobis distance values.

When I re-ran the analysis using an **R** matrix scaled for population size, different results were obtained (Figure 7.6). Kaminaljuyu plotted far away from the central cluster of sites, and the Pacific Coast sample plotted closer to the other Maya sites, but still as an outlier. Also, Calakmul and Tikal moved to the edge of the main cluster of Maya sites. A review of Table 7.17 indicates that this is due to an increased biological distance between these two sites

Table 7.16. Classic Maya genetic distances derived from the unscaled **R** matrix.

	Tikal	Calak-mul	Piedras Negras	Altar	Seibal	Dos Pilas	Altun Ha	Barton Ramie	Colha	Copan	KJ
Calakmul	0.0182										
Piedras Negras	0.0190	0.0466									
Altar	0.0818	0.0771	0.0959								
Seibal	0.0611	0.1398	0.0838	0.1152							
Dos Pilas	0.0371	0.0000	0.0486	0.0540	0.1116						
Altun Ha	0.0006	0.0578	0.0175	0.0540	0.0401	0.0617					
Barton Ramie	0.1192	0.0946	0.1407	0.1029	0.0505	0.0612	0.1119				
Colha	0.0010	0.0000	0.0581	0.0983	0.1163	0.0291	0.0355	0.1005			
Copan	0.0177	0.0224	0.0712	0.0736	0.0619	0.0267	0.0457	0.0756	0.0137		
Kaminal-juyu	0.1110	0.0727	0.1200	0.0842	0.1351	0.0402	0.1042	0.0929	0.0917	0.1379	
Pacific Coast	0.1100	0.1252	0.0226	0.2430	0.2364	0.1317	0.1452	0.3485	0.1689	0.1524	0.3265

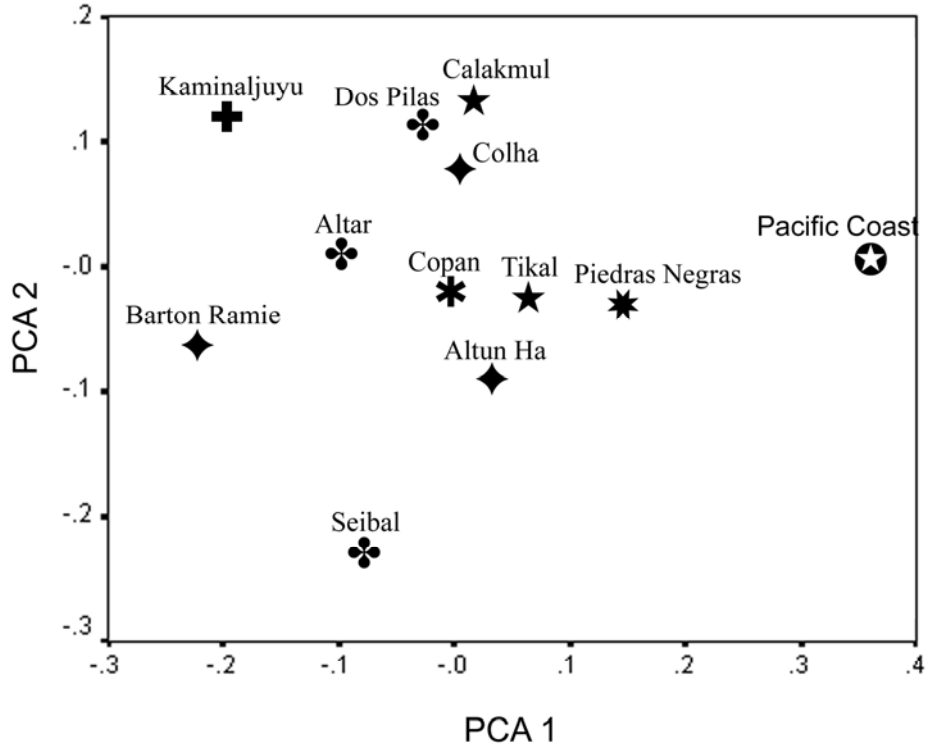

Figure 7.5. Principal components plot of Classic Maya sites based on unscaled **R** matrix. Archaeological Zones: Central (★), Pasión (✤), Usumacinta (✸), Belize (✦), Southeast (✱), Highlands (✚).

Table 7.17. Classic Maya genetic distances derived from the scaled **R** matrix.

	Tikal	Calak-mul	Piedras Negras	Altar	Seibal	Dos Pilas	Altun Ha	Barton Ramie	Colha	Copan	KJ
Calakmul	0.0597										
Piedras Negras	0.0111	0.0297									
Altar	0.0264	0.0107	0.0141								
Seibal	0.0342	0.1442	0.0460	0.0457							
Dos Pilas	0.0467	0.0000	0.0171	0.0042	0.0633						
Altun Ha	0.0000	0.0555	0.0065	0.0091	0.0256	0.0267					
Barton Ramie	0.0611	0.0304	0.0356	0.0171	0.0254	0.0128	0.0309				
Colha	0.0105	0.0000	0.0220	0.0106	0.0698	0.0135	0.0163	0.0248			
Copan	0.0256	0.0275	0.0373	0.0162	0.0376	0.0191	0.0282	0.0225	0.0124		
Kaminal-juyu	0.1627	0.0912	0.0965	0.0628	0.1113	0.0527	0.0927	0.0622	0.0938	0.1439	
Pacific Coast	0.0374	0.0410	0.0080	0.0547	0.1040	0.0449	0.0509	0.0991	0.0610	0.0613	0.2031

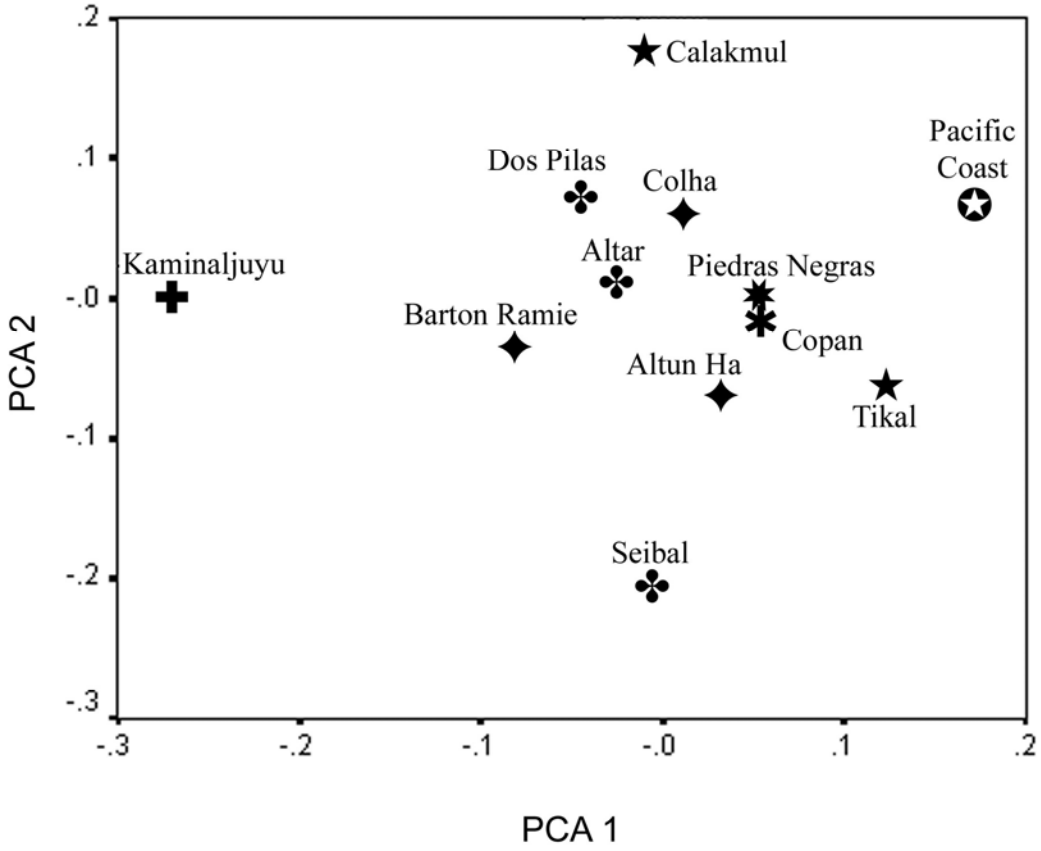

Figure 7.6. Principal components plot of Classic Maya sites based on scaled **R** matrix. Archaeological Zones: Central (★), Pasión (✤), Usumacinta (✸), Belize (✦), Southeast (✱), Highlands (✚).

(0.0597), though their respective distances with the other Maya sites in the analysis are largely unchanged from the unscaled **R** matrix analysis. In general, there is a trend for sites with larger population sizes to cluster to the edge or outside of the main cluster of sites. Clearly, effective population size has some effect on dental variability in the Maya area.

As a final evaluation of both the validity of the **R** matrix analysis and of the original data imputation method on which all of the multivariate dental metric analyses in this chapter were based, I performed multiple **R** matrix analyses using different imputed datasets. In addition to the original imputation of missing data, I ran four more imputations to produce a total of five different dental metric datasets. I performed an unscaled **R** matrix analysis using each of the five dental metric datasets. From these analyses, I produced four new genetic distance matrices. I then used a Mantel test to compare the original **R** matrix intersite genetic distance matrix (Table 7.16) to each of the four new distance matrices.

Table 7.18 shows that all of the Mantel tests were significant. This demonstrates a strong correlation between the distance matrix produced from the original imputed data set and the distance matrices produced from the alternative imputed data sets. This verifies the validity of the data imputation procedure—alternative imputations produce the same results in the multivariate biological distance analyses.

SUMMARY

Overall, there was substantial dental metric homogeneity in the Maya area during the Classic Period. This was first indicated by ANOVA and MANOVA and confirmed by the Mahalanobis Distance analysis, for which only one pair-wise comparison was significant. **R** matrix analysis generated low F_{ST} values, further indicating a relative lack of between-site

Table 7.18. Results of four Mantel tests comparing the **R** matrix distance matrix from the original imputed dataset to the **R** matrix distance matrices derived from four alternative imputed datasets.

Alternative Imputations	r^2	p
Dataset 1	.1813	.031
Dataset 2	.5370	.001
Dataset 3	.5462	.001
Dataset 4	.2898	.004

variation in dental metric traits. These results indicate dental metric variability was minimal between Classic Maya sites. This suggests that either substantial gene flow prevented regional differentiation in the area or, assuming a common origin for Maya populations, that not enough time was available for genetic drift to produce regional variation in dental size.

Unfortunately, unavoidable decisions in the research design may have affected the results. The pooling of males and females prevented sex-specific analyses that might have been more equipped to identify inter-site differences. Second, the imputation of data for multivariate analyses required a dramatic reduction in sample size. As a result, some sites were representated by a very small sample of individuals (~10) who may not have been representative of the site's overall dental variation.

With these caveats in mind, a few observations can be made. The multivariate analyses indicated a closer affinity amongst lowland Maya sites relative to the highland site of Kaminaljuyu, and the Pacific Coast. In the Pasión Zone, Altar de Sacrificios and Seibal were separated from the other Maya sites, but did not show strong affinity to one another. Similarly, Dos Pilas did not demonstrate phenotypic affinity to the other Pasión sites, but rather was loosely affiliated with Calakmul. Tikal and Piedras Negras demonstrated some affinity, though Piedras Negras was also an outlier, especially in the PCA plot. In the Belize Zone, very little association was demonstrated amongst the sites.

CHAPTER VIII

DISCUSSION AND CONCLUSIONS

In this chapter, I compare the results of the multivariate analyses of the dental metric and nonmetric data to the research hypotheses proposed in Chapter III. I establish that dental nonmetric and metric data are suitable for studying ancient Maya population history and structure. All of the analyses indicate that Maya population structure does not follow isolation by distance model. Rather, extensive gene flow between Maya sites characterized the Classic period. I explore how the biological data, in conjunction with the archaeological and hieroglyphic record, can answer specific questions pertaining to ancient Maya population history.

RESEARCH HYPOTHESES

Hypothesis #1: Classic Maya populations exhibit among-group genetic variabilty and this variability can be meaningfully measured by phenotypic differences in dental nonmetric and metric data.

The results of the dental nonmetric analysis support this hypothesis. Using the log likelihood ratio test, I found moderate levels of dental nonmetric heterogeneity in the Maya area, with between 14% and 50% of Maya traits exhibiting statistically significant differences between Maya sites. When I analyzed the nonmetric traits using a standardized Mean Measure of Divergence (MMD) analysis, 72.7% of the pairwise distance values (40/55) were statistically significant (Table 6.7). When I excluded the sites with problematic sample sizes—Copan,

Colha, and Kaminaljuyu—the number of statistically significant pairwise values increased to 82.1% (23/28). These results indicate that dental nonmetric data is an appropriate tool for reconstructing ancient Maya population history.

Previous research on Maya dental nonmetrics generally confirms these results. In his comparison of dental nonmetric variability between Tipu and select other Maya sites, Jacobi (2000: 179) found that 38.9% (14/36) of his standardized MMD values were statistically significant. Rhoads (2002: 211) compared her dental nonmetric data from the Maya site of Copan to nine other sites in the Maya area and elsewhere in Latin America. She found that 43.6% (24/55) of her pairwise distance values were statistically significant. However, Rhoads used unstandardized MMD distances for which a different criterion is used to identify statistical significance than that used in this study. Wrobel compared dental nonmetric variability between three sites in northern Belize, two sites in the central Petén, and one site in the Yucatán. He indicates that the MMD values he reports are standardized (Wrobel 2003: 152), but just how this was accomplished is unclear in his methodology (Wrobel 2003: 124). If the MMD values are indeed standardized, then none of his pairwise values are significant by Sjøvold's (1973) criterion. However, Wrobel does not specifically discuss the statistical significance of his results. Thus, I hesitate to draw any conclusions about the statistical significance of Wrobel's findings.

With the exception of Wrobel's study, previous work in Maya dental nonmetrics found moderate levels of varaibility between sites. In comparison to these studies, I report a high abundance of statistically significant intersite differences. I attribute the higher percentage of statically significant pairwise values in this study to my use of a Maya-specific nonmetric trait dichotomization scheme. In contrast, all of the other studies used Turner's (1986) breakpoints. Turner's breakpoints were devised for addressing large scale patterns in dental variability around

the world. By using a Maya-specific trait dichotomization scheme, I was able to identify subtle variations in trait expressions between sites that might have otherwise been missed.

Determining whether the dental metric data varies significantly between Maya sites is more complicated, since a number of different multivariate tests were used to examine variability in dental metrics across the Maya area. The results of the ANOVA, Levene's test, and MANOVA indicate relative homogeneity in dental metrics among Maya sites. Moreover, in the Mahalanobis distance analysis; none of the pairwise distance values were significant.

In Wrobel's (2003) study of dental metric variation in northern Belize, he also found that the majority of his univariate comparisons of tooth size between sites produced statistically insignificant results. For his multivariate comparisons, Wrobel used Penrose size and shape coefficients with varying degrees of success, and he does not report the statistical significance of those results. In their analysis of dental metric variability among select sites in the Yucatán, southeast Petén, and Belize, Cucina and Tiesler (2004) report low intersite dental metric variability when individual measurements are considered, although they do not describe their statistical methods. They did not perform tests of significance on their multivariate analyses.

Do the results presented here, and those from other studies of Maya dental metrics, indicate that tooth dimensions are inappropriate for reconstructing population history in the Maya area? The **R** matrix analysis can help clarify this issue. Williams-Blangero and Blangero (1989) have shown that the **R** matrix distances represent minimum genetic distances. The genetic distances obtained in this study are similar to those found in Stojanowski's (2004) regional study of colonial period missions in the American southeast, the only other dental metric study that uses the **R** matrix approach, to my knowledge. This suggests that although dental metrics are an extremely conservative tool for reconstructing population history, they still can be used to elucidate patterns in biological variability. This is underscored when the plot of

the unscaled **R** matrix analysis (Figure 7.5) is compared to that derived from the PCA (Figure 7.3) and Mahalanobis distance (Figure 7.4) analyses. All three plots show the same general pattern of biological affinity, with subtle variation in the smallest clustering of sites.

As a final consideration, I compare the results of dental metric and nonmetric data to each other. Interestingly, the two methods do not produce the same results. Some consistencies are noted. For instance, in both the nonmetric and metric analyses, Piedras Negras demonstrates relatively large biological distances from the other Maya sites and has its closest affinity—albeit distant—with Tikal. Another consistent pattern is that Altar de Sacrificios and Seibal do not cluster with other lowland sites. However, other relationships are fundamentally different. In the nonmetric MMD analysis, Barton Ramie and Calakmul possess a small pairwise distance, whereas in the dental metric analyses they demonstrate very little affinity.

A number of factors may be contributing to the seeming inconsistencies between these two measures. First, the dental metric data is based on a reduced number of individuals. Although the analysis began with approximately the same set of individuals for the metric and nonmetric analyses, because of the requirements for data imputation, individuals with few observable teeth were excluded from the dental metric analyses. Second, dental nonmetrics were found to be far more variable among Maya sites than dental metrics. This is underscored in the differences between the two dimensional plots of the nonmetric and metric analyses. In the MDS plots of the MMD analysis, the sites are scattered away from the centroid, especially in the plot that excludes the sites with problematic sample sizes (Figure 6.4). In contrast, the majority of the sites cluster near the centroid in the metric plots.

To my knowledge, all other studies that use both dental metric and nonmetric data report a similar phenomenon. Powell (1995: 226) found significant variability among middle Holocene samples using dental nonmetric data, whereas the dental metric data were not particularly

variable among the samples. Wrobel (2003: 170) also found dental nonmetric data to have greater variability among groups, whereas differences in his dental metric data were associated with time. Although I found no time trend in the Tikal data, it remains a possibility for the other sites. However, I have controlled for temporal trends in the data by limiting my samples to the Classic period, with the majority of the skeletons from the Late or Terminal Classic periods. Although Rhoads (2002) used both dental metric and nonmetric data in her analysis, she does not comment on the utility of one versus the other and does not use the dental metric data for intersite comparisons, largely because she lacked comparative dental metric data for other sites.

If dental nonmetric data are indeed the more variable of the two kinds of phenotypes, it raises interesting questions regarding the evolutionary nature of discrete versus quantitative traits. Scott and Turner (1997) contend that dental nonmetric traits are highly conservative to evolutionary change. Yet studies that use both dental nonmetric and metric data often find that nonmetric traits are more variable among groups. Although beyond the scope of this dissertation, this is an issue that needs to be addressed in future studies of dental nonmetric and metric data.

Based on these observations, I feel hypothesis #1 can be accepted, with caution. Ancient Maya populations are phenotypically variable. Nonetheless, I exercise caution in developing my conclusions, considering the differences between the two datasets. For whatever reasons, the results obtained from the dental nonmetric analysis are not precisely the same as those achieved for the metric data. This may be due to sampling error, or it may reflect differences in the sensitivity to evolutionary changes of the two datasets as noted above.

One possible source of error that remains untested is the possible affects of sex. Dental metric data are affected by sex. Unfortunately, sex-effects could not be controlled for in this analysis due to the difficulty of sexing ancient Maya skeletons. Nonetheless, if the samples did

not contain equal numbers of males and females and/or if one of the sexes was more mobile than the other, then it is possible that among-group heterogeneity may be under- or overestimated with the dental metric data.

Hypothesis #2: Classic Maya population structure can be explained by an isolation by distance model.

The results of both the dental nonmetric and metric analyses demonstrate that Hypothesis #2 should be rejected; there is not a clear association between biological distance and geographic distance. Using Mantel tests between geographic distance and biological distances, I found a lack of association in all cases, for both dental nonmetric and metric analyses. In the dental nonmetric analyses, sites did not cluster by archaeological zone. Although Altar de Sacrificios and Seibal have a small biological distance between them in the MMD analysis, the third Pasión site, Dos Pilas, does not demonstrate an affinity with these sites. In the dental metric analyses, none of the archaeological zones of the Maya lowlands formed identifiable clusters. However, the geographically outlying sites of Kaminaljuyu and the Pacific Coast were also outliers in the biological distance analyses. The dental metric analyses thus point towards greater gene flow amongst lowland Maya sites, and reduced gene flow between lowland sites and Kaminaljuyu and the Pacific Coast. In this respect, that data indicates that isolation by distance is valid when sites beyond the Maya lowlands are considered.

The results of the **R** matrix analysis also indicate substantial intersite gene flow within the Maya area. F_{ST} was used to measure among group variation in the Maya area. When all of the sites are considered, an F_{ST} value of 0.018 was obtained. This value is low when compared to other regional studies of genetic differentiation based on quantitative traits. Comparably low

F_{ST} values were reported for precontact sites from the Georgia Coast (F_{ST} = 0.008, Stojanowski 2004) and modern Jirel villages in Nepal (F_{ST} = 0.010, Williams-Blangero and Blangero 1989). These all represent cases of little regional differentiation among populations, indicating that gene flow, rather than drift, was the dominant evolutionary force affecting population structure in these areas. Larger levels of genetic differentiation were observed in the late precontact Illinois River valley (F_{ST} = 0.028, Steadman 2001), in the precontact Ohio Valley (F_{ST} = 0.078, Tatarek and Sciulli 2000), amongst 19th century Iroquois (F_{ST} = 0.053, Langdon 1995), 19th century Algonquian speakers (F_{ST} = 0.055, Jantz and Meadows 1995), 19th century northern Pacific populations (F_{ST} = 0.109, Ousley 1995), and modern Ireland (F_{ST} = 0.027, Relethford and Blangero 1990). Interestingly, the F_{ST} for the Classic Maya area is nearly the same as that obtained for Mississippian populations of the Illinois River Valley, another New World, sedentary, complex society (F_{ST} = 0.010, Steadman 2001). Framed from this perspective, it is clear that gene flow, not population isolation and drift, characterized Classic period Maya population structure.

If gene flow was greater among sites within archaeological zones than among sites compared between zones, F_{ST} values would be smaller in each archaeological zone relative to F_{ST} estimates for the entire area. This is true for the Central Zone (F_{ST} = 0.003), however both the Pasión Zones (F_{ST} = 0.018) and the Belize Zones (0.019) exhibit values roughly the same as the F_{ST} estimate for the entire region. In other words, the sites of the Central Zone exhibit less among group variability than those of either the Belize or Pasión zones, where greater among group genetic differentiation was observed.

A consideration of the Relethford-Blangero analysis clarifies the F_{ST} values. Most of the sites exhibit residuals near zero (Table 7.12). This indicates that the majority of sites in this analysis were part of a shared network of gene flow. The exceptions are Seibal, Barton Ramie,

and Kaminaljuyu. These three sites are responsible for the increased among group variability, and raised the minimum F_{ST} values. These sites appear to have received emigrants from sites beyond the Maya area, or from Maya sites that were not sampled here. Barton Ramie is one possible exception, due to its small population. When I ran the scaled **R** matrix analysis, which accounts for drift on small population sizes, Barton Ramie, which was formerly an outlier in the biological distance analyses, clustered closer to the other Maya sites (Figure 7.6). This indicates that the separation between Barton Ramie and the other Maya sites in the other multivariate analyses was due to the effects of genetic drift on the small population of Barton Ramie.

POPULATION HISTORY

The analysis of dental nonmetric and metric variability in the Maya area has shown that an isolation by distance model does not adequately describe ancient Maya population structure. Further, the **R** matrix analysis has demonstrated that gene flow between Maya sites dominated population structure, with population isolation and genetic drift being relatively weak during the Classic period. With this in mind, I turn to specific questions relevant to Maya population history to determine if historical events proposed from the archaeological and epigraphic records may help clarify the results of the biological analyses and inform us about population history in the Maya area.

Central Zone

- *As the major Classic period superpowers, did the large sites of Tikal and Calakmul experience high levels of gene flow with other parts of the Maya world?*

In the dental nonmetric analyses, Tikal and Calakmul both demonstrate statistically significant pairwise distance with most other sites in the analysis. Overall, Tikal does not

demonstrate an affinity to any site. Calakmul has relatively small pairwise distances with Barton Ramie, Colha, Copan, and Kaminaljuyu. However, the latter three sites have small sample sizes and, thus, might be unstable in the MMD analysis. The association between Calakmul and Barton Ramie was unexpected and is not easily explained. Perhaps there was considerable gene flow between Barton Ramie and the Central Petén, or between Calakmul and Belize. Alternatively, genetic drift of the small Classic period population of Barton Ramie may have affected phenotypic variability at the site. The results of the **R** matrix analysis support the latter conclusion; the Barton Ramie population was subject to genetic drift.

In the dental metric analyses, Tikal and Calakmul were centrally located in the plots of biological distance. In the **R** matrix analysis, the Central Zone—comprised of Tikal and Calakmul—produced a very small F_{ST} (0.0031) indicating very little genetic differentiation between the two sites. In contrast, the **R** matrix analyses of the Belize Zone and the Pasión Zone produced higher F_{ST} values. By adding either Calakmul or Tikal to either of these respective **R** matrix analyses actually reduces their F_{ST}. In other words, much of the genetic variation between sites of the Belize Zone or between sites of the Pasión Zone, is present within the populations of Tikal and Calakmul. This is likely due to the large population size and large intrasite genetic variability at both Tikal and Calakmul.

Although the data from Tikal and Calakmul appear to indicate low between-site genetic differentiation in the Central Zone, this observation needs to be confirmed with data from additional Central Zone sites. Cucina and Tiesler (2004) compared dental metric variability at Calakmul to sites in Southeastern Petén and the Yucatán. They found that Calakmul consistently clustered with the southeastern Petén sites, providing further evidence for biological affinity amongst Central Zone sites.

Interestingly, in the scaled **R** matrix analysis, which accounts for genetic drift, the separation between Calakmul and Tikal increases, with both sites, particularly Calakmul, separating from the remaining Maya sites (Figure 7.6). When the genetic distance matrix is examined (Table 7.17), it is clear that the separation of Tikal and Calakmul is the result of a large biological distance between these two sites, even though the distance between these sites and most other sites is relatively small. Thus, when all of the biological data on Tikal and Calakmul are considered, it appears that these were two large, relatively heterogeneous sites. Although they were were biologically separated from one another, both had ties to other Maya sites. In other words, there likely was not substantial gene flow between Calakmul and Tikal, though both sites may have exchanged genes with the same lesser sites in the Central Zone. That fact the ceramics of Calakmul and Tikal were relatively similar in the Late Classic (Rice and Forsyth 2003: 36), supports this observation. Although endemic conflict likely resulted in little direct interaction between Tikal and Calakmul, they indirectly exchanged material culture, ideas, and even genes through interaction with lesser sites in the Central Zone.

These results make sense in light of recent interpretations of Classic Maya politics (Martin and Grube 1995, 2000). Most Mayanists now agree that by the Late Classic period, Tikal and Calakmul were hegemonic powers overseeing a complex network of alliances and enmities. These networks were apparently fluid, depending on the waxing and waning fortunes of each of the superpowers. Perhaps the best example comes from the site of Dos Pilas, which was founded with the support of Tikal but was later subjugated by Calakmul (Fahsen 2003). Further, the Late Classic ceramic similarity between Tikal and Calakmul indicates that they were involved in some of the same trade networks (Braswell, et al. 2004), though the antagonism between the two likely inhibited direct interaction. Nonetheless, it is important to keep in mind that the Calakmul dental sample in this study may not be representative of the whole site, with a

possible bias towards elite individuals. In contrast, the Tikal sample clearly comes from more heterogeneous mortuary contexts.

Usumacinta Zone

- *Can the population explosion at Piedras Negras be explained by immigration from the Central Zone?*

Houston and colleagues (2003) raised the possibility that late Early Classic population growth at Piedras Negras was caused by an influx of immigrants from the central Petén. The biological data provides some support for this hypothesis. In the dental nonmetric analysis, Piedras Negras was isolated from other sites. Although Piedras Negras grouped with Tikal in the dendogram, the affinity between the two is not particularly strong. In the dental metric analyses, Piedras Negras was relatively isolated in the PCA and unscaled **R** matrix analyses. In the Mahalanobis distance analysis, Piedras Negras clustered with other Maya sites, particularly Tikal and Colha. A small pairwise biological distance between Tikal and Piedras Negras was also observed in the unscaled **R** matrix analysis.

These results indicate that the Classic period Piedras Negras population was relatively isolated from populations in other regions of the Maya area. Nonetheless, Piedras Negras' strongest affinity is with the central Petén site of Tikal. Based on these analyses, I favor Golden and colleagues (2003) proposal that the Classic period population explosion at Piedras Negras and other primate centers in the Usumacinta Zone was due to an influx of local populations, not tested here. However, the loose affinity to the site of Tikal indicates that some genetic interaction may have occurred between the two at some point in their history.

In the scaled **R** matrix analysis, Piedras Negras clusters with other sites in the Maya area. These results indicate that a significant portion of the genetic variability observed at

Piedras Negras, relative to Maya other sites, was the result of genetic drift. Although the F_{ST} values indicate that gene flow, not drift, dominated the genetic structure of the Maya area, it appears that the Usumacinta Zone, more so than other parts of the Maya lowlands area, was genetically isolated. The Sierra del Lacandón Mountains form a formidable barrier separating much of the Usumacinta Zone from the rest of the Maya area to the east. The major routes of travel into and out of the area were along the Usumacinta River and the valleys that parallel it (Anaya 2001). In terms of least cost of travel, the nearest sites to Piedras Negras in this study are those of the Pasión region. However, these sites show no particular affinity to Piedras Negras. This is not surprising when the archaeological and epigraphic record is considered. In regards to ceramics, Piedras Negras is relatively isolated from other parts of the Maya area, particularly during the Late Classic period (Rice and Forsyth 2004). Late Classic period ceramic styles are distinct in the Usumacinta Zone and elite, codex-style polychromes, typical of the Central Zone, are rare in the Usumacinta Zone. The hieroglyphic evidence indicates the majority of Piedras Negras' political interaction was with other sites in the western Maya area (Schele 1991), none of which are sampled here.

Pasión Zone

- *Was the Late Classic Dos Pilas population comprised of immigrants from the site of Tikal?*

The biological data is surprisingly ambiguous about the origins of the Dos Pilas population. The dental nonmetric analysis suggests a loose affinity between the Pasión sites of Altar de Sacrificios and Seibal, with Dos Pilas as an outlier. In the dental metric analysis, Dos Pilas remains an outlier and Altar de Sacrificios and Seibal do not demonstrate any affinity to one another. In fact, Dos Pilas does not demonstrate a particularly strong affinity to any of the other sites in this study. These results most likely indicate a mixed origin for the population of

Dos Pilas. The settlement patterns at Dos Pilas are most like those at Seibal (Houston 1993). In general, the ceramics of Dos Pilas are similar to other Petexbatun sites, though at the elite level Dos Pilas was importing a large quantity of elite polychromes from the Central Petén (Foias personal communication, 2004). Unfortunately, samples from other Petexbatun sites with Early Classic components—Arroyo de Piedra and Tamarindito—were excluded due to their small sample sizes. With this in mind, I suggest that the majority of the population at Dos Pilas had indigenous origins with an elite class imposed from the central Petén site of Tikal. However, this interpretation relies far more on the archaeological and epigraphic data, than on clear evidence from the biological data. Dos Pilas shares its emblem glyph with Tikal (Houston 1993) and the epigraphic record indicates that the site was founded by members of Tikal's royal family (Houston 1993; Martin and Grube 2000), with support from its king (Fahsen 2003).

Interestingly, Dos Pilas has a small pairwise distance with the site of Calakmul in the dental metric analyses. This was unexpected since the founding lineage is known to be from Tikal, not Calakmul (Houston 1993). This may suggest that following the defeat of Dos Pilas by Calakmul and its political re-alignment into the Calakmul hegemony (Fahsen 2003), gene flow occurred between the two sites—perhaps through marriage networks or the permanent settlement of Calakmul elites at Dos Pilas. However, there is no archaeological or epigraphic evidence, aside from known visits of Calakmul ambassadors at Dos Pilas (Houston 1993; Martin and Grube 2000), to support this proposition. Rather, the majority of the documented marriages for the Dos Pilas' king were with women from other sites in the Pasión.

- *Was the Terminal Classic renaissance at Seibal and Altar de Sacrificios due to an influx of individuals from outside the Pasión Zone?*

During the Terminal Classic period, Seibal underwent fluorescence at a time when many of its neighbors went into decline. Based on stylistic differences in ceramics and sculpture, researchers have variously proposed an invasion of foreigners from the Gulf Coast region (Sabloff 1973; Sabloff and Willey 1967) or new leadership sent from the Petén site of Ucanal (Schele and Matthews 1998). The biological data provide compelling evidence for a Terminal Classic population infusion at Seibal. The dental nonmetric data indicate that Seibal shows a strong biological affinity to the nearby site of Altar de Sacrificios but is otherwise distinct from the other sites in the study. However, the dental metric biological distance analyses show Seibal to be biologically distinct from all other sites in the sample. Why Seibal does not cluster with Altar in the dental metric analyses, but does in the nonmetric analyses is unclear. It may reflect differences in the evolutionary nature of dental metrics or could be due to sampling error, since the dental metric analyses are based on a reduced set of individuals. Even when the possible affects of genetic drift are considered in the scaled **R** matrix analysis, Seibal remains an outlier. The Relethford-Blangero analysis indicates that Seibal received greater than average external gene flow from populations outside of those sampled here during the Classic period.

In a similar analysis of dental nonmetric variability, Austin (1978) found biological discontinuity between his early sample (Preclassic to Late Classic periods) and late sample (Terminal Classic period) at Seibal, whereas at Altar, he found biological continuity. His results support those here; gene flow led to an increase in biological variability at Seibal. Jacobi (2000) compared Austin's early and late samples to dental nonmetric data from other Maya sites and found that the two Seibal samples clustered with different sites in his analysis, though the biological distance between the early and late samples is not statistically significant. When the results of my study are considered in light of Austin and Jacobi's finding, it appears that there is evidence of external gene flow at Seibal during the Classic period.

Unfortunately, the timing of that gene flow cannot be precisely identified, though Austin and Jacobi's findings suggest it occurred around the Late to Terminal Classic period transition. Further, these analyses cannot be used to clarify the origins of the immigrants. The Putun Maya from the Gulf Coast, the invaders originally proposed by the Seibal project, certainly would have been outside of the mating networks considered in this analysis and gene flow from these groups could account for the high residuals observed in the Relethford-Blangero analysis. However, recent interpretations discount much of the evidence for a Gulf Coast invasion at Seibal (Tourtellot and González 2004). Rather, Tourtellot and Gonzalez argue for an indigenous fluorescence, sponsored by Wat'ul Chatel, a Terminal Classic leader sent from Ucanal. Apparently, Wat'ul Chatel arrived with a sizable population, enough to alter the genetic structure of Seibal's Classic period population. Unfortunately, without comparative biological data from Ucanal, I cannot confirm whether or not this site was the source of the immigrants.

Belize Zone

- *Does the cultural variability of Belize correspond to biological differences between sites of this zone?*

In both the dental nonmetric and metric analyses, the Belizean sites demonstrated little affinity to one another. The variability in the Belizean group was underlined by its F_{ST} value of 0.0189 which, although small, was the largest obtained for any combination of sites in this analysis. In the dental nonmetric analyses, Altun Ha and Barton Ramie had a small pairwise biological distance. However, no affinity between these two was identified in the dental metric analyses. In the dental nonmetric analyses, Barton Ramie demonstrated an affinity to the site of Calakmul, whereas in the dental metric analyses it was relatively isolated from other sites. I suspect these seemingly conflicting results are due genetic drift at Barton Ramie. Barton Ramie

had a small population size and was a very minor site with no major elite occupation. As a site of little significance, Barton Ramie demonstrates very little archaeological evidence for interaction with other Maya sites, particularly from other regions. In fact, it is Barton Ramie's absence of an elite class and a lack of dependency on larger Maya centers to the west that may have allowed it to survive the Maya collapse (Fry 1990).

The Belizean biological data indicates substantial genetic heterogeneity in the zone. Similarly, the Belize Zone exhibited a diversity of ceramic styles during during the Classic period (Rice and Forsyth 2004). For instance, in northern Belize, the immediate area around Colha exhibits distinctly different ceramics than the rest of the zone (Rice and Forsyth 2004). At Colha, the ceramics show strong affinities to the Tepeu sphere of the Central Petén (Valdez 1987). Interestingly, when the dental nonmetric data are considered, Colha shows a loose affiliation with Tikal, though caution must be taken due to Colha's small sample size in the nonmetric analysis. In the metric analyses, Colha repeatedly demonstrates small pairwise distances with the Central Petén sites of Tikal and Calakmul. This raises the possibility that some segment of the Colha population may have been migrants from the Central Zone or that they shared a common origin. However, it is important to keep in mind that the majority of the Colha skeletal sample comes from the Operation 2011 skull pit. The identity of these individuals remains unknown (Barrett and Scherer 2004; Massey and Steele 1997; Mock 1994). They may have been captured from elsewhere and sacrificed at Colha, or they may have been local residents of the site who were killed. I favor the latter hypothesis because the skull pit contains children (unlikely foreign war captives), is contemporaneous with another major deposit of mutilated human remains (Operation 2012), and coincides with the Terminal Classic abandonment of the site. Nonetheless, the biological and ceramic evidence raise the possibility

that Classic period Colha was partly occupied by immigrants from the Central Petén, or that gene flow regularly occurred between Colha and that region.

Southeast Zone

- *Can the Classic period population boom at Copan be explained by immigration from either Tikal or Kaminaljuyu?*

Researchers have linked Early Classic period at Copan with possible immigration from either the Central Petén (Longyear 1952) or Kaminaljuyu (Valdés and Wright 2004). Alternatively, Fash and Stuart (1991) have proposed that the Classic period tradition at Copan was a product of local Ch'olan Maya populations who had been in the area since the Preclassic period with little to no foreing immigration.

In both the dental nonmetric and metric analyses, Copan clustered with the other Maya sites, even though it lies on the geographic periphery of the Maya area. In the Relethford-Blangero Analysis, Copan had a negative residual, indicating less than average gene flow from outside the area of sites included in the Relethford-Blangero analysis. This suggests that the Classic period Copan population was not receiving substantial immigrants from non-Maya peoples of Mesoamerica. Rather, Copan appears to have regularly received gene flow from other parts of the Maya area.

The dental nonmetric data allude to a biological affinity between Copan and Kaminaljuyu. However, I hesitate to make any conclusions based on these results since both Copan and Kaminaljuyu have problematic sample sizes in the nonmetric MMD analysis. In the dental metric analyses, Copan and Kaminaljuyu are distinct from one another, with large pairwise distances. This indicates that there is very little biological affiliation between Classic

period Copan and Classic period Copan. However, in Valdés and Wright's (2004) proposed immigration, the immigrants were from Preclassic Kaminaljuyu, not the Classic period population. Popenoe de Hatch (2002) believes that Kaminaljuyu was resettled, or at least taken over, by invaders from the western highlands. If she is correct, then the Preclassic and Classic period Kaminaljuyu populations may have been genetically distinct. Thus, I argue that no definitive conclusions regarding a Copan-Kaminaljuyu connection can be made based on the dental metric data.

The dental nonmetric data indicate a connection between Copan and the Central Petén, particularly the site of Calakmul. However, the small size of the Copan sample may be skewing the results and I hesitate to derive any interpretations from these results. More informative are the dental metric data. In these analyses, Copan repeatedly demonstrates an affinity to the Central Zone, with the strongest affinity to the site of Tikal. These data could be taken as evidence of a large scale Classic period migration to Copan. However, the archaeological, hieroglyphic, and isotopic data suggest a more complex process. Rather than wholesale immigration into the Copan valley, the present consensus is that the Early Classic founder of Copan's dynasty, Yax K'uk' Mo' was a foreigner from the Central Petén (Stuart 2004). Prior to Yax K'uk Mo's arrival, Copan shows greater archaeological affinity to general southeastern traditions (Canuto 2004; Sharer 2003; Sharer, et al. 1999). However, after his arrival, Copan grew into one of the great Maya powers, demonstrating all of the characteristics of Classic Maya culture (Sharer 2004). Evidence of Copan's Early Classic connection to the Central Petén comes from the Acropolis tombs, which are rich in ceramics, many of which bear strong stylistic similarities to Tikal and the more distant Central Mexican site of Teotihuacan (Bell, et al. 2004). Some of these vessels were actually manufactured in the Tikal area (Reents-Budet, et al. 2004). Further, the bones that are believed to be Yax K'uk' Mo's have an isotopic signature consistent

with the Central Petén (Buikstra, et al. 2004). Nonetheless, there is no evidence of major Central Petén immigration at Copan. Rather, Yax K'uk' Mo' likely arrived with an entourage of followers (Sharer 2004: 300), and Copan's subsequent alliance with Tikal may have resulted in a steady stream of interaction and presumably gene flow between the two.

Highlands

- *Was the cultural exchange between the highland site of Kaminaljuyu and Tikal and Copan accompanied by gene flow between the two areas?*

The biological distance analyses are ambiguous in regard to the issue of genetic exchange between Kaminaljuyu and other parts of the Maya area. The nonmetric analyses suggest substantial gene flow between Kaminaljuyu and all of the sites tested. Low pairwise distance values were found, and Kaminaljuyu was centered in the multidimensional scaling plot (Figure 6.3), though with a lack of affinity to other sites. However, the sample size for Kaminaljuyu in the nonmetric analyses is problematic and may be affecting the results.

In contrast, the dental metric analyses suggest very little biological affinity between Kaminaljuyu and the other Maya sites. In all of the analyses, Kaminaljuyu demonstrated large biological distances from other sites. This lack of association is especially apparent for Tikal and Copan, which have large pairwise distance values with Kaminaljuyu. The Relethford-Blangero analysis found a high, positive residual for Kaminaljuyu, indicating substantial gene flow with populations outside this study area, or with sites not sampled here.

One possibility is that some component of the Classic period population at Kaminaljuyu was from Teotihuacan (Kidder, et al. 1946; Sanders 1977). However, recent stable isotope analyses (Valdés and Wright 2004; White, et al. 2000) and reviews of the archaeological data (Demarest and Foias 1993) indicate that a Teotihuacan presence at Kaminaljuyu was small or

non-existent (Braswell 2003). However, the stable isotope evidence did identify secondary individuals in the Early Classic tombs that were foreigners, either from the Petén or the Pacific Coast (Valdés and Wright 2004; White, et al. 2000).

Based on ceramic evidence, Popenoe de Hatch (2002) proposed a major population incursion at Kaminaljuyu at the Preclassic-Early Classic transition. She suggests that these invaders came from the west, originating from somewhere in Chiapas. The data here support Popenoe de Hatch's hypothesis in that the Classic period population of Kaminaljuyu was biologically distinct from other Classic period Maya sites and had received genetic material from outside the area. In addition to gene flow from invaders, admixture may also have been occurring with other highland populations or Pacific coast populations not sampled here.

Pacific Coast

- *Was the Pacific Coast comprised of populations with biological affiliations to the Maya lowlands and highlands?*

The size of the Pacific Coast sample was too small to permit its use in the dental nonmetric analyses. However, the dental metric analyses indicate that the Pacific Coast sample used here was biologically divergent from Maya populations in the lowlands, as well as from the highland site of Kaminaljuyu. In all analyses, the Pacific Coast sample demonstrated large biological distances from the other sites. The one exception is the scaled **R** matrix analysis, which results in the Pacific Coast exhibiting relatively small pairwise distances to the other samples. This analysis accounts for the possible affects of population size and indicates that genetic drift could have produced the variation seen. These results are not surprising since the Pacific Coast was assigned an extremely small population rank based on the available settlement data and may not be accurate. When I rescaled the Pacific Coast population rank to a size

comparable to the Maya centers of Piedras Negras and Dos Pilas, the Pacific Coast sample diverged from the other Maya sites, similar to that observed in the unscaled **R** matrix analysis. These results indicate that the Pacific Coast is biologically distinct from the Maya lowlands, but with overlapping genetic variation.

The biological data make sense in light of the archaeological evidence. Of all the samples included in this analysis, the Pacific Coast series—comrpised of the sites of Balberta and the Montana Complex—is the most culturally divergent. It was not part of a pure Classic Maya tradition. Rather, the Pacific coast of Guatemala and Chiapas was its own vibrant region, with connections to the highlands, the Gulf Coast, and El Salvador. In addition, a strong connection to Central Mexico has been documented, and Bove and Medrano (2003) argue that Teotihuacanos were present on the Pacific Coast, particularly at the Montana Complex. Thus, it is not surprising that the Pacific Coast is distinct from the lowland Maya area—there is a large geographic separation between the two and the Pacific Coast exhibits networks of interaction with other regions that may not have involved lowland Maya populations.

CONCLUSIONS AND FUTURE RESEARCH

This dissertation demonstrated that (1) dental metric and nonmetric analyses can be used to reconstruct population history in the Maya area, (2) isolation by distance does not describe Classic Maya population structure, rather (3) extensive gene flow dominated Classic period population structure and some of the episodes of ancient population interaction can be identified in the bioarchaeological record.

Both dental nonmetric and metric data proved valuable in exploring ancient Maya population variability. The dental nonmetric data demonstrated substantial diversity among Classic Maya sites. The dental metric data demonstrated less variability. These differences have

been noted in previous studies that incorporate both dental nonmetric and metric data (Powell 1995; Wrobel 2003). For the dental metric analysis, I was able to use a number of both model-free and model-bound approaches. Principal components analyis, Mahalanobis distance analysis and **R** matrix analysis all produced remarkably similar results. This underscores the strength of using a both approaches to the study of ancient population dynamics. In this study, the model-bound **R** matrix analysis was able to highlight the possible effects of population size and biological variability amongst the Classic Maya. Yet the model-free approaches, which make far fewer theoretical assumptions, confirmed many of the results of the model-bound analysis. Future studies of ancient population history and structure will benefit from using both approaches.

This research is the tip of the iceberg. As new ancient Maya skeletal samples become available and statistical methods for studying ancient population variability become more refined, new and exciting avenues of investigation will open up. In particular, further attention needs to be paid to both chronological changes in population structure within the Classic period and to the presence of sub-populations within Maya sites, particularly between social classes. The major site of Tikal, with its large skeletal sample, presents ample opportunity to explore these issues and integrate the population data with ongoing archaeological and osteological research at the site. Research is also needed to explore differences between male and female gene flow within and between Maya sites. The methodology for exploring post-marital settlement patterns in bioarchaeology is well established (Konigsberg 1988; Lane and Sublett 1972; Spence 1974a); the challenge lies in amassing a sufficiently large dental sample of reliably-sexed skeletal remains to perform the analysis.

This research has underscored the dynamic nature of Maya populations and has shed new light on some of the most intriguing questions in Maya archaeological. Further, it has

shown that biological distance analyses remain a viable and interesting tool for the study of ancient populations. In particular, this research has shown that the use of both model-free and model-bound approaches are relevant for studying ancient population history, and this complementary approach results in more robust interpretations than if only one of this approaches was followed.

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APPENDIX A

TOOTH ABBREVIATIONS

UI1 -- Upper First Incisor
UI2 -- Upper Second Incisor
UC -- Upper Canine
UP3 -- Upper First Premolar
UP4 -- Upper Second Premolar
UM1 -- Upper First Molar
UM2 -- Upper Second Molar
UM3 -- Upper Third Molar

LI1 -- Lower First Incisor
LI2 -- Lower Second Incisor
LC -- Lower Canine
LP3 -- Lower First Premolar
LP4 -- Lower Second Premolar
LM1 -- Lower First Molar
LM2 -- Lower Second Molar
LM3 -- Lower Third Molar

APPENDIX B

ARIZONA STATE UNIVERSITY DENTAL ANTHROPOLOGY SYSTEM:

TRAITS, GRADES OF EXPRESSION, AND DESCRIPTIONS[1]

Winging (UI)
0. Straight[2]
1. Bilateral Winging
2. Unilateral Winging
3. Counter-Winging

Shoveling (UI1, UI2, UC, LI1)
0. None
1. Faint
2. Trace
3. Semishovel
4. Semishovel
5. Shovel
6. Marked shovel
7. Barrel (UI2 only)

Labial Convexity (UI1)
0. Labial surface is flat
1. Labial surface exhibits trace convexity
2. Labial surface exhibits weak convexity
3. Labial surface exhibits moderate convexity
4. Labial surface exhibits pronounced convexity

Double Shoveling (UI1, UI2, UC, UP1)
0. None
1. Faint
2. Trace
3. Semi-double-shovel
4. Double-shovel
5. Pronounced double-shovel
6. Extreme double-shovel

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[1] All traits and grades of expression are from Turner et al. 1991.

[2] In Turner et al. 1991, *straight* is classified as "3," however I it was more logical to treat this grade as "0" as it represents the absence of this trait. *Counter- winging*, which is scored here as "3," was scored by Turner et al. as "4."

Interruption Groove (UI1, UI2)

0. None
M. An interruption groove occurs on the mesio-lingual border.
D. An interruption groove occurs on the disto-lingual border.
MD. Grooves occur on both the mesio- and disto-lingual borders.
Med. A groove occurs in the medial area of the cingulum.

Tuberculum Dentale (UI1, UI2, UC)

0. No expression
1. Faint ridging
2. Trace ridging
3. Strong ridging
4. Pronounced ridging
5. Weakly developed cuspule
6. Strong cusp with a free apex

Canine Medial Ridge (UC)

0. Mesial and distal lingual ridges are the same size
1. Mesiolingual ridge is larger than the distolingual, and is weakly attached to the tuberculum dentale.
2. Mesiolingual ridge is larger than the distolingual, and is moderately attached to the tuberculum dentale.
3. Morris's type form. Mesiolingual ridge is much larger than the distolingual, and is full incorporated into the tuberculum dentale.

Canine Distal Accessory Ridge (UC, LC)

0. Distal accessory ridge is absent.
1. Distal accessory ridge is very faint.
2. Distal accessory ridge is weakly developed.
3. Distal accessory ridge is moderately developed.
4. Distal accessory ridge is strongly developed.
5. Distal accessory ridge is very pronounced.

Premolar Mesial and Distal Accessory Cusps (UP1, UP2)

0. No accessory cusps occur.
1. Mesial and/or distal accessory cusps are present.

Tricusped Premolars (UP3, UP4)

0. Extra distal cusp (hypocone) is absent.
1. Hypocone is present

Distosagittal Ridge (UP1)

0. Normal premolar form occurs.
1. Distosagittal ridge is present.

Metacone (UM1, UM2, UM3)

0. Metacone is absent.
1. An attached ridge with no free apex
2. A faint cuspule with a free apex
3. Weak cusp
3.5. Intermediate-sized cusp
4. Metacone is large.
5. Metacone is very large

Hypocone (UM1, UM2, UM3)

0. No hypocone
1. Faint ridging
2. Faint cuspule
3. Small cusp
3.5. Moderate-sized cusp
4. Large cusp
5. Very large cusp.

Cusp 5 (Metaconule) (UM1, UM2, UM3)

0. Absent
1. Faint cuspule
2. Trace cuspule
3. Small cuspule.
4. Small cusp
5. Medium-sized cusp

Carabelli's Trait (UM1, UM2, UM3)

0. Absent
1. Groove
2. Pit
3. Small Y-shaped depression
4. Large Y-shaped depression
5. Small cusp without a free apex
6. Medium-sized cusp
7. Large free cusp

Parastyle (UM1, UM2, UM3)

0. Absent
1. Pit
2. Small cusp
3. Medium-sized cusp
4. Large cusp
5. Very large cusp
6. Free peg-shaped crown attached to the root

Premolar Lingual Cusp Variation (LP3, LP4)

A. No lingual cusp
0. One lingual cusp
1. One or two lingual cusps
2. Two lingual cusps: Mesial cusp is much larger than distal cusp
3. Two lingual cusps: Mesial cusp is larger than distal cusp
4. Two lingual cusps: Mesial and distal cusps are equal in size
5. Two lingual cusps: Distal cusp is larger than mesial cusp
6. Two lingual cusps: Distal cusp is much larger than mesial cusp
7. Two lingual cusps: Distal cusp is very much larger than mesial cusp
8. Three lingual cusps: Each is about the same size
9. Three lingual cusps: Mesial cusp is much larger than medial and/or distal cusp

Anterior Fovea (LM1, LM2, LM3)

0. Absent
1. Weak ridge, faint groove
2. Stronger ridge, larger groove
3. Groove is longer than in grade 2
4. Groove is very long and mesial ridge is robust

Groove Pattern (LM1, LM2, LM3)

Y. Cusps 2 (metaconid) and 3 (hypoconid) are in contact
+. Cusps 1-4 (protoconid, metaconid, hypoconid, entoconid) are in contact
X. Cusps 1 (protoconid) and 4 (entoconid) are in contact

Cusp Number (LM1, LM2, LM3)

4. Cusps 1-4 (1, protoconid; 2, metaconid; 3, hypoconid; 4, entoconid) are present
5. Cusp 5 (hypoconulid) is also present
6. Cusp 6 (entoconulid) is also present

Deflecting Wrinkle (LM1, LM2, LM3)

0. Absent
1. Cusp 2 medial ridge is straight, but with midpoint constriction
2. Medial ridge is deflected distally, does not contact cusp 4
3. Medial ridge is deflected distally forming an L-shaped ridge and contacts cusp 4

Distal Trigonid Crest (LM1, LM2, LM3)

0. Absent
1. Present

Protostylid (LM1, LM2, LM3)

0. Absent
1. Pit
2. Buccal groove curves distally
3. Faint secondary groove extends mesially
4. Secondary groove is slightly more pronounced
5. Secondary groove is stronger
6. Weak or small cusp
7. Cusp with a free apex occurs

Cusp 5 (Hypoconulid) (LM1, LM2, LM3)

0. Absent
1. Very small
2. Small
3. Medium-sized
4. Large
5. Very large

Cusp 6 (Entoconulid) (LM1, LM2, LM3)

0. Absent
1. Cusp 6 is much smaller than cusp 5
2. Cusp 6 is smaller than cusp 5
3. Cusp 6 is equal in size to cusp 5
4. Cusp 6 is larger than cusp 5
5. Cusp 6 is much larger than cusp 5

Cusp 7 (Metaconulid) (LM1, LM2, LM3)

0. Absent
1. Faint cusp

1A. A faint tipless cusp

2. Small
3. Medium-sized
4. Large

Enamel Extensions (UP3, UP4, UM1, UM2, UM3, LP3, LP4, LM1, LM2, LM3)

0. Absent
1. Faint
2. Medium-sized
3. Large

Tomes' Root (LP3)

0. Absent
1. Shallow V-shaped groove
2. Moderately deep V-shaped groove
3. Deep V-shaped groove
4. Deep groove on both mesial and distal borders
5. Two free roots are present

Root Number (UP3, UP4, UM1, UM2, UM3, LP3, LP4, LM1, LM2, LM3)

1. One root
2. Two roots
3. Three roots
4. Four roots

Radical Number (UP3, UP4, UM1, UM2, UM3, LP3, LP4, LM1, LM2, LM3)

1. One radical
2. Two radicals
3. Three radicals
4. Four radicals
5. Five radicals
6. Six radicals
7. Seven radicals
8. Eight radicals

Peg shaped Incisor (UI2)

0. Normal sized incisor
1. Incisor reduced in size, but having normal crown form
2. Peg-shaped incisor

Peg shaped Molar (UM3)

0. Normal sized molar
1. Molar reduced in size to 7 to 10 mm buccolingual diameter
2. Molar is <7 mm in buccolingual diameter

Odontome (UP3, UP4, LP3, LP4)

0. Absent.
1. Present.

Congenital Absence (UI2, LI1, UP3, LP4, UM3, LM3)

0. Tooth is present
1. Congenitally absent

Torsomolar Angle (LM3)[3]

0. No rotation.
1. 1°-19° rotation, buccally.
2. 1°-19° rotation, lingually.
3. 20°-45° rotation, buccally.
4. 20°-45° rotation, lingually.
5. >45° rotation, buccally.
6. >45° rotation, lingually.

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[3]Numerical classification was created to facilitate statistical calculations.
Turner et al. (1991) recommend simply recorded the angle and direction of the rotation.

VITA

Andrew Kenneth Scherer was born on July 6, 1976 in St. Cloud Minnesota. He attended St. John's Preparatory School in Collegeville, Minnesota and graduated in 1994. He attended Macalester College from the fall of 1994 through the fall of 1995. Andrew transferred to Hamline University in the spring of 1996 and graduated summa cum laude in the spring of 1998 with a Bachelor of Arts degree with Honors in Anthropology and minors in American Indian Studies, Geology, and Religious Studies. While at Hamline University, Andrew assisted with osteological analysis relating to NAGPRA.

Andrew entered graduate school in the fall of 1998 at Texas A&M University. While at Texas A&M, Andrew studied bioarchaeology, Maya archaeology, and population genetics. Andrew assisted Lori Wright in her osteological analysis of the human remains from Tikal, Guatemala; served as project osteologist on the Piedras Negras Archaeological Project; and conducted a skeletal analysis of the human remains from Operation 2011 of Colha, Belize. In 2003, Andrew became Assistant Director of the Sierra del Lacandón Regional Archaeology Project in Guatemala. Andrew was a Laboratory Instructor for "Introduction to Physical Anthropology" at Texas A&M University and Lecturer for "Introduction to Physical Anthropology" at Baylor University. He worked as a Kenyon Team Member at the Office of Chief Medical Examiner, City of New York in response to the World Trade Center Disaster and the crash of American Airlines Flight 587.

In addition to numerous research reports, Scherer has co-authored articles pertaining to ancient Maya osteology and mortuary practices that have appeared in *Latin American Antiquity*, *Ancient Mesoamerica*, and *Antropología de La Eternidad*.

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